

Gencore version 5.1.4\_P5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Run on: March 18, 2003, 23:07:15 ; Search time 991 seconds  
(without alignments)  
293.671 Million cell updates/sec

Title: US-09-702-498a-33-MOD  
Perfect score: 10  
Sequence: 1 CuuuCACCCu 10

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Genbank:  
 1: gb\_bat:\*  
 2: gb\_hhg:\*  
 3: gb\_in:\*  
 4: gb\_om:\*  
 5: gb\_ovr:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pl:\*  
 9: gb\_pr:\*  
 10: gb\_ro:\*  
 11: gb\_sis:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_v1:\*  
 15: em\_ba:\*  
 16: em\_fun:\*  
 17: em\_hum:\*  
 18: em\_in:\*  
 19: em\_mu:\*  
 20: em\_on:\*  
 21: em\_or:\*  
 22: em\_ovr:\*  
 23: em\_potc:\*  
 24: em\_ph:\*  
 25: em\_pi:\*  
 26: em\_ro:\*  
 27: em\_sts:\*  
 28: em\_v1:\*  
 29: em\_vn:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pin:\*  
 35: em\_htg\_rnd:  
 36: em\_htg\_man:  
 37: em\_htg\_vct:  
 38: em\_sy:  
 39: em\_htg\_hum:  
 40: em\_htg\_mus:  
 41: em\_htg\_other:

## ALIGNMENTS

RESULT 1  
AX134713  
LOCUS AX134713  
DEFINITION Sequence 1 from Patent WO0132898.  
ACCESSION AX134713  
VERSION AX134713.1 GI:14271230  
KEYWORDS SOURCE  
ORGANISM synthetic construct  
ARTIFICIAL  
SEQUENCES

REFERENCE 1 (bases 1 to 10)

AUTHORS Yonemitsu, Y., Hasagawa, M. and Alton, E.

TITLE Recombinant sendai virus vector for introducing exogenous genes to

airway epithelia

PATENT: WO 0132898-A 1 10-MAY-2001;

Pred. No. is the number of results predicted by chance to have a

**FEATURES source** Dnavec Research Inc. (JP) Location/qualifiers  
 1..10  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="artificially synthesized sequence"

**BASE COUNT** 1 a 5 c 0 g 4 t  
**ORIGIN**

**RESULT 2**  
**Query Match** 100.0%; Score 10; DB 6; Length 10;  
**Best Local Similarity** 60.0%; Pred. No. 2.1e+05;  
**DEFINITION** Matches 6; Conservative 4; Mismatches 0;  
**LOCUS** Indels 0; Gaps 0;  
**QY** 1 CUUUCACCCU 10  
**Db** 1 CTTTACCCCT 10

**KEYWORDS**

**SOURCE** synthetic construct.

**ORGANISM** synthetic construct.

**REFERENCE** 1.10

**AUTHORS** Griesenbach, U., Ferrari, S., Geddes, D.M., Alton, E.W., Hasegawa, M.  
 and Hou, X.

**TITLE** Paramyxovirus vector for gene transfer to the cardiovascular system  
 JOURNAL Patent: WO 0230726-A 1 16-MAY-2002;

**FEATURES** Location/Qualifiers

source /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Artificially Synthesized Sequence"

**BASE COUNT** 1 a 5 c 0 g 4 t  
**ORIGIN**

**RESULT 3**  
**Query Match** 100.0%; Score 10; DB 6; Length 10;  
**Best Local Similarity** 60.0%; Pred. No. 2.1e+05;  
**DEFINITION** Matches 6; Conservative 4; Mismatches 0;  
**LOCUS** Indels 0; Gaps 0;  
**QY** 1 CUUUCACCCU 10  
**Db** 1 CTTTACCCCT 10

**KEYWORDS**

**SOURCE**

**ORGANISM**

**REFERENCE** 1.10

**AUTHORS** Bennett, C. Frank, and Vickers, T.A.

**TITLE** Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
 JOURNAL Patent: US 6077833-A 5 20-JUN-2000;

**FEATURES** Location/Qualifiers

source /organism="unknown"

**BASE COUNT** 4 a 6 c 0 g 5 t  
**ORIGIN**

**RESULT 4**  
**Query Match** 100.0%; Score 10; DB 6; Length 12;  
**Best Local Similarity** 60.0%; Pred. No. 2.1e+05;  
**DEFINITION** Matches 6; Conservative 4; Mismatches 0;  
**LOCUS** Indels 0; Gaps 0;  
**QY** 1 CUUUCACCCU 10  
**Db** 11 CTTTACCCCT 2

**KEYWORDS**

**SOURCE**

**ORGANISM** Unknown.

**REFERENCE** 1.12

**AUTHORS** Wang, C.-G. and Hepburn, A.G.

**TITLE** Genetic sequence assay using DNA triple strand formation  
 JOURNAL Patent: US 5861244-A 23 19-JAN-1999;

**FEATURES** Location/Qualifiers

source /organism="unknown"

**BASE COUNT** 5 a 0 c 6 g 1 t  
**ORIGIN**

**RESULT 5**  
**Query Match** 100.0%; Score 10; DB 6; Length 12;  
**Best Local Similarity** 60.0%; Pred. No. 2.1e+05;  
**DEFINITION** Matches 6; Conservative 4; Mismatches 0;  
**LOCUS** Indels 0; Gaps 0;  
**QY** 1 CUUUCACCCU 10  
**Db** 12 CTTTACCCCT 3

**KEYWORDS**

**SOURCE**

**ORGANISM** Unknown.

**REFERENCE** 1.19

**AUTHORS** Bennett, C. Frank, and Vickers, T.A.

**TITLE** Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
 JOURNAL Patent: US 6077833-A 5 20-JUN-2000;

**FEATURES** Location/Qualifiers

source /organism="unknown"

**BASE COUNT** 4 a 6 c 0 g 5 t  
**ORIGIN**

**RESULT 6**  
**Query Match** 100.0%; Score 10; DB 6; Length 19;  
**Best Local Similarity** 60.0%; Pred. No. 1.9e+05;  
**DEFINITION** Matches 6; Conservative 4; Mismatches 0;  
**LOCUS** Indels 0; Gaps 0;  
**QY** 1 CUUUCACCCU 10  
**Db** 7 CTTTACCCCT 16

**KEYWORDS**

**SOURCE**

**ORGANISM**

**REFERENCE** 1.11

**AUTHORS** Blum, K., Noble, E.P. and Sheridan, P.J.

**TITLE** Allelic association of the human dopamine(D2) receptor gene in compulsive disorders  
 JOURNAL Patent: US 5500343-A 1 19-MAR-1996;

**FEATURES** Location/Qualifiers

source /organism="unknown"

**BASE COUNT** 4 a 0 c 6 g 1 t  
**ORIGIN**

**Query Match** 100.0%; Score 10; DB 6; Length 11;



				PC	C12N15/86,C12N15/45//A61K31/7105,A61K48/00
				CC	Description of Artificial Sequence: artificially synthesized
				primer	
				CC	
				sequence	
QY	1	CUUUCACCCU	10	FH	
Db	11	CTTTCACCC	20	FEATURES	Location/Qualifiers
				source	1..21
RESULT 11					/organism="synthetic construct"
BD013048/C	BD013048	21 bp	DNA	linear	PAT 02-AUG-2002
LOCUS	BD013048				DEFINITION
ACCESSION	BD013048				Paramyxovirus having modified transcription initiation sequence.
VERSION	BD013048.1				GI:22093237
KEYWORDS	WO 0118223-A/11.				
SOURCE					synthetic construct.
ORGANISM					synthetic construct.
REFERENCE					artificial sequences.
AUTHORS	Nagai,Y., Kato,A. and Hasegawa,M.				
TITLE	Paramyxovirus having modified transcription initiation sequence				
JOURNAL	Patent: WO 0118223-A 11 15-MAR-2001;				
COMMENT	DNA/VEC RESEARCH INC,YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA				
PN	WO 0118223-A/11				OS Artificial Sequence
PD	15-MAR-2001				ID BD010081/C
PF	06-SEP-2000	WO 2000JP006051			ID BD010081
PR	06-SEP-1999	JP 99P 25231			AC BD010081;
.PI	YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA				XX
PC	C12N15/86,C12N15/45//A61K31/7105,A61K48/00				SV BD010081.1
CC	Description of Artificial Sequence: artificially synthesized primer.				XX
CC	sequence				XX
FEATURES	Key Location/Qualifiers				DT 08-FEB-2002 (Rel. 70, Created)
source	1..21				DT 08-FEB-2002 (Rel. 70, last updated, Version 1)
BASE COUNT	/db_xref="taxon:32630"				DE Paramyxovirus having modified transcription initiation sequence.
ORIGIN	4 a 4 c 6 g 7 t				XX
QY	1 CUUUCACCCU	10			KW JP 03075813-T/11.
Db	13 CTTTCACCC	4			XX
RESULT 12					OS synthetic construct.
LOCUS	BD013049	21 bp	DNA	linear	OC artificial sequence.
DEFINITION	Paramyxovirus having modified transcription initiation sequence.				XX
ACCESSION	BD013049				RN [1]
VERSION	BD013049.1				RP 1..21
KEYWORDS	WO 0118223-A/12.				RA Nagai Y., Kato A., Hasegawa M.;
SOURCE					RT Paramyxovirus having modified transcription initiation sequence";
ORGANISM					RL Patent number JP03075813-T/11, 06-MAR-2001.
REFERENCE	1 (bases 1 to 21)				RL DNA/VEC RESEARCH INC,YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.
AUTHORS	Nagai,Y., Kato,A. and Hasegawa,M.				XX
TITLE	Paramyxovirus having modified transcription initiation sequence				CC OS Artificial Sequence
JOURNAL	Patent: WO 0118223-A 12 15-MAR-2001;				CC PN JP 03075813-T/11.
COMMENT	DNA/VEC RESEARCH INC,YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA				CC PD 06-MAR-2001
OS	Artificial Sequence				CC PP 06-SEP-2000 JP 2000006051
PN	WO 0118223-A/12				CC PR 06-SEP-1999 JP 99P 25231
PD	15-MAR-2001				CC PI YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA
PF	06-SEP-2000	WO 2000JP006051			CC PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00
PR	06-SEP-1999	JP 99P 25231			CC CC C12N15/86,C12N15/45//A61K31/7105,A61K48/00
PI	YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA				CC CC F1 Key
COMMENT	1 CUUUCACCCU	10			CC CC FT source
OS	Artificial Sequence				CC CC FT 1..21
PN	WO 0118223-A/12				CC CC FT /db_xref="taxon:32630"
PD	15-MAR-2001				CC CC FT /organism="synthetic construct"
PF	06-SEP-2000	WO 2000JP006051			XX SQ Sequence 21 BP; 4 A; 4 C; 6 G; 7 T; 0 other;
PR	06-SEP-1999	JP 99P 25231			Query Match 100.0%; Score 10; DB 23; Length 21;
PI	YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA				BEST Local Similarity 60.0%; Pred. No. 1.9e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY	1 CUUUCACCCU	10			
Db	11 CTTTCACCC	20			

Db 13 CTTTCACCC 4

RESULT 14

ID BD010082 standard; DNA; SYN; 21 BP.

XX BD010082;

XX BD010082.1

SV

XX

DT 08-FEB-2002 (Rel. 70, Created)

DE Parainfluenza virus having modified transcription initiation sequence.

XX JP 03075813-T/12.

XX

OS synthetic construct.

OC artificial sequence.

XX

RN [1]

RA Nagaai Y., Kato A., Hasegawa M.;

RT "Parainfluenza virus having modified transcription initiation sequence";

RL Patent number JP03075813-T/12, 06-MAR-2001.

RNAVEC RESEARCH INC, YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.

XX

CC OS Artificial Sequence

CC PN JP 03075813-T/12

CC PD 06-MAR-2001

CC PR 06-SEP-2000 JP 2000006051

CC PT 06-SEP-1999 JP -99P 232231

CC PI YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA

CC PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00

CC CC

CC FH Key Location/Qualifiers

CC FT source 1..21

CC FT /organism="Artificial Sequence"

XX FH

FT Key Location/Qualifiers

FT source 1..21

FT /db\_xref="taxon:32630"

FT /organism="synthetic construct"

XX

SQ Sequence 21 BP; 7 A; 6 C; 4 G; 4 T; 0 other;

Query Match Best local Similarity 60.0%; Score 10; DB 23; Length 21;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10

!:::|||||:

Db 9 CTTCACCC 18

RESULT 15

AR099567

LOCUS AR099567

DEFINITION Sequence 94 from patent US 6077833. DNA linear PAT 14-FEB-2001

ACCESSION AR099567

VERSION AR099567.1 GI:12809333

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)

AUTHORS Bennett,C, Frank and Vickers,T.A.

TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein

JOURNAL Patent: US 6077833-A 94 20-JUN-2000;

FEATURES Location/Qualifiers

source	1..22
	/organism="unknown"
BASE COUNT	6 a 6 c 5 g 5 t
ORIGIN	
Query Match	100.0%; Score 10; DB 6; Length 22;
Best Local Similarity	60.0%; Pred No. 1.9e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Matches	
QY	1 CUUUCACCCU 10
Db	10 CTTTCACCC 19

Search completed: March 19, 2003, 00:40:37  
Job time : 991 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1\_4\_p5\_4578  
copyright (c) 1993 - 2003 Compugen Ltd.

## On nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:06:05 ; Search time 168 Seconds  
(without alignments)  
134.048 Million cell updates/sec

Title: US-09-702-498a-33-MOD  
Perfect score: 100.0  
Sequence: CuuucACCCu 10  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : Listing first 45 summaries

N\_Geneseq\_101002.\*

1: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1980.DAT.\*  
2: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1981.DAT.\*  
3: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1982.DAT.\*  
4: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1983.DAT.\*  
5: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1984.DAT.\*  
6: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1985.DAT.\*  
7: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1986.DAT.\*  
8: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1987.DAT.\*  
9: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1988.DAT.\*  
10: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1989.DAT.\*  
11: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1990.DAT.\*  
12: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1991.DAT.\*  
13: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1992.DAT.\*  
14: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1993.DAT.\*  
15: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1994.DAT.\*  
16: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1995.DAT.\*  
17: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1996.DAT.\*  
18: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1997.DAT.\*  
19: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1998.DAT.\*  
20: /STDSD2/gcadata/geneseq/geneseqn-embl/NA1999.DAT.\*  
21: /STDSD2/gcadata/geneseq/geneseqn-embl/NA2000.DAT.\*  
22: /STDSD2/gcadata/geneseq/geneseqn-embl/NA2001A.DAT.\*  
23: /STDSD2/gcadata/geneseq/geneseqn-embl/NA2001B.DAT.\*  
24: /STDSD2/gcadata/geneseq/geneseqn-embl/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	10 22	AAT5896 Nucleotide sequence, SBO DNA sequence, SBO S Sequence Oligo
2	10	100.0	10 22	AAT73613 Sendai virus S seq
3	10	100.0	22	AAT23653 Modified transcript
4	10	100.0	10 22	AAT86115 Sendai virus S seq
5	10	100.0	10 22	AAT77598 Sendai virus S seq
6	10	100.0	10 24	AAT42656 Angiostrongylus gene
7	10	100.0	10 24	AAT38107 DNA sequence #1 re
8	10	100.0	10 24	ABR48812 Sendai virus S oligo
9	10	100.0	10 24	ABU39904 Sendai virus S oligo

C	10	100.0	11 15	AAQ57929 Oligonucleotide #1
C	11	100.0	11 17	AAT18122 Human dopamine D2
C	12	100.0	12 20	AAJ14846 Triple helix form I
C	13	100.0	13 23	ABF08726 Oligonucleotide SE
C	14	100.0	13 23	ABF08727 Oligonucleotide SE
C	15	100.0	13 23	ABH24716 Oligonucleotide SE
C	16	100.0	13 23	ABH24717 Oligonucleotide SE
C	17	100.0	14 22	AAF77602 Modified transcript
C	18	100.0	14 22	AAF77603 Modified transcript
C	19	100.0	14 22	AAF77605 Modified transcript
C	20	100.0	15 22	AAF70291 Human DRD2 allele
C	21	100.0	15 22	AAF70292 Human DRD2 allele
C	22	100.0	15 22	AAF70389 Human DRD2 allele
C	23	100.0	15 22	AAF70391 Human DRD2 allele
C	24	100.0	17 24	ABK57674 Human CCL1 gene e
C	25	100.0	17 24	ABK57675 Human CCL1 gene e
C	26	100.0	17 24	ABK57570 Human CCL1 gene e
C	27	100.0	17 24	ABK57571 Human CCL1 gene e
C	28	100.0	19 19	AAV8056 Human B7-2 targett
C	29	100.0	19 22	AAV2898 Human B7-2 mRNA an
C	30	100.0	21 22	AAV6495 PCR primer MIG173
C	31	100.0	21 22	ABK68004 PCR primer MIG173
C	32	100.0	21 22	AAF77592 Modified transcript
C	33	100.0	21 22	AAF77592 Human B7-2 targett
C	34	100.0	21 22	AAK97290 Human gene single
C	35	100.0	21 24	ABK50521 PCR primer #1 for
C	36	100.0	21 24	ABK10908 Human familial com
C	37	100.0	21 24	ABK68004 Human FCHL1 locus
C	38	100.0	22 19	AAV48055 Human B7-2 targett
C	39	100.0	22 22	AAV2897 Human B7-2 mRNA an
C	40	100.0	22 23	AAQ62986 Angiotensinogen mo
C	41	100.0	23 19	AAV23970 Primer for detecti
C	42	100.0	23 21	AAZ0307 PCR primer used to
C	43	100.0	23 21	AAZ38437 Human angiotensino
C	44	100.0	23 22	AAE57107 Human angiotensino
C	45	100.0	24 22	AAE070469 Human DRD2 exon 6

## ALIGNMENTS

RESULT 1	ID	XX	XX	XX
AA165896	AA165896 standard; DNA; 10 BP.			
AA165896;				
03-JAN-2002	(first entry)			
XX	Nucleotide sequence of a synthetic oligonucleotide.			
XX	Vaccine; Sendai virus vector; viral protein; immunodeficiency virus; AIDS; antigen gene; nasal mucosa; lymph node; ss.			
XX	Synthetic.			
OS				
XX	W0200172340-A1.			
PD	04-OCT-2001.			
XX				
PF	30-MAR-2001; 2001WO-JP02769.			
PR	30-MAR-2000; 2000US-193127P.			
PA	(DNAV-) DNAYEC RBS INC.			
PA	(NINA-) JAPAN NAT INST INFECTIOUS DISEASES.			
XX	Kano M., Matano T., Kato A., Nagai Y., Hasegawa M;			
DR	WPI; 2001-616443/71.			
XX				
PT	viral protein of immunodeficiency virus-encoding Sendai virus vector-based AIDS virus vaccine for provision of efficient protective			

PT immunity comprises nasal administration to e.g. macaque to suppress  
 PT onset and progress of AIDS  
 XX Disclosure; Page 27; 92pp; Japanese.

PS

XX The specification describes a vaccine containing a sendai virus vector  
 CC which encodes the viral protein of immunodeficiency virus. The vaccine  
 CC is for treating AIDS, with expression of antigen gene mediated by the  
 CC vector in nasal mucosa and local lymph nodes detected and  
 CC antigen-specific cell-mediated responses induced at significant  
 CC level after vaccination. The present sequence represents an  
 CC oligonucleotide which is used in the course of the invention.

XX

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4 2e+03; Mismatches 0;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cuuucacccu 10  
 Db 1 CTTCACCCP 10

RESULT 2

AAH73613  
 ID AAH73613 standard; DNA; 10 BP.  
 XX  
 AC AAH73613;  
 XX  
 DT 27-SEP-2001 (first entry)  
 DE DNA sequence, SEQ ID NO: 1.  
 XX  
 KW Gene therapy; vascular disorder; recombinant paramyxovirus vector; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200153491-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PR 11-JAN-2001; 2001WO-JP00087.  
 XX  
 PR 19-JAN-2000; 2000JP-0014136.  
 XX  
 PA (DNAV-) DNAVEC RBS INC.  
 XX  
 PI Masaki I, Yonemitsu Y, Sueishi K, Hasegawa M, Kinoh H;  
 XX DR WPI; 2001-457610/49.  
 XX  
 PT Paramyxovirus vector containing foreign gene for efficient gene  
 PR transfer into vascular cells -  
 XX  
 PS Disclosure; Page 19; 84pp; Japanese.

XX The invention relates to a method for inserting nucleic acid into blood  
 CC vessel cells by contacting the cells with the nucleic acid contained in a  
 recombinant paramyxovirus vector or cells transformed by it. The  
 CC method can be used for gene therapy of vascular disorders. Genes that  
 CC can be introduced into blood vessel cells by this method include cell  
 cycle regulators (such as p53, p21, p16 and p27), inhibitory factors  
 CC (such as R-Ras, eNOS and C-natriuretic peptide), ion channels (such as  
 CC Kir 6.2 potassium channel), blood proteins (such as urokinase and  
 CC tissue plasminogen activator), tissue factor pathway inhibitors (such  
 CC as TFPI) and vascular growth factors (such as vascular endothelial  
 CC growth factor (VEGF), fibroblast growth factor (FGF) and hepatocyte  
 CC growth factor (HGF)). The present sequence is provided in the  
 XX specification.

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4 2e+03; Mismatches 0;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cuuucacccu 10  
 Db 1 CTTCACCCP 10

RESULT 3

AAH23653  
 ID AAH23653 standard; DNA; 10 BP.  
 XX  
 AC AAH23653;  
 XX  
 DT 07-AUG-2001 (first entry)  
 DE S. sequence oligonucleotide used in a recombinant Sendai virus vector.  
 XX  
 KW Gene therapy; S sequence; airway epithelium; cystic fibrosis; ds.  
 XX  
 OS Parainfluenza virus.  
 XX  
 PN WO200132898-A2.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 02-NOV-2000; 2000WO-JP07737.  
 XX  
 PR 02-NOV-1999; 99US-0163055.  
 XX  
 PR 17-DEC-1999; 99JP-0359218.  
 XX  
 PA (DNAV-) DNAVEC RBS INC.  
 XX  
 PI Yonemitsu Y, Hasegawa M, Alton EW;  
 XX DR WPI; 2001-328799/34.  
 XX  
 PT New chorioallantoic fluid containing a recombinant Sendai virus vector  
 PT carrying an exogenous gene, useful in gene therapy, particularly for  
 PT treating cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep,  
 PT bovine or monkey -  
 XX  
 PS Disclosure; Page 7; 42pp; English.

XX The present invention relates to a composition for introducing exogenous  
 CC genes to airway epithelia. The composition comprises a recombinant Sendai  
 CC virus vector carrying an exogenous gene. The composition is useful in  
 CC gene therapy. In particular, the composition is useful for treating  
 CC cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep, bovine or  
 CC monkey. The present sequence was used in the composition of the present  
 CC invention as a transcription start sequence.

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4 2e+03; Mismatches 0;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cuuucacccu 10  
 Db 1 CTTCACCCP 10

RESULT 4

AAF86115  
 ID AAF86115 standard; DNA; 10 BP.  
 XX  
 AC AAF86115;  
 XX  
 DT 21-JUN-2001 (first entry)  
 DE Sendai virus S sequence oligonucleotide.

SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

XX  
 KW Extracellular superoxide dismutase; EC-SOD; immunosuppressive;  
 KW antiinflammatory; antiarthritis; antirheumatic; arthritis; colitis;  
 KW Systemic autoimmune disease; systemic lupus erythematosus;  
 KW rheumatic carditis; progressive systemic sclerosis; dermatomyositis;  
 KW Sjogren's syndrome; polyarteritis; Sendai virus; ss.  
 XX OS Parainfluenza virus.  
 XX CA2316518-Al.  
 XX PD 01-MAR-2001.  
 XX PA (DNAV-) DNA VEC RES INC.  
 XX PF 31-AUG-2000; 2000CA-2316518.  
 XX PR 01-SEP-1999; 99JP-0248032.  
 XX PR 27-AYR-2000; 2000CA-2304453.  
 XX PA (DNAV-) DNA VEC RES INC.  
 XX DR WPI; 2001-244576/25.  
 XX XX Paranyxovirus vectors with modified transcription initiation sequences  
 XX PT for increased expression of foreign genes in production of drugs and  
 XX PT vaccines.  
 XX PI Nagai Y, Kato A, Hasegawa M;  
 XX DR WPI; 2001-244576/25.  
 XX XX Disclosure: Page 17; 65pp; Japanese.  
 XX CC The present invention describes a paranyxovirus vector DNA in which the  
 CC transcription initiation sequence has been modified to modify the  
 CC expression of a gene located downstream of the transcription initiation  
 CC sequence. This is useful in the production of mutant paranyxovirus  
 CC vectors with elevated gene expression and a more rapid proliferation than  
 CC the wild-type vector, which can then be used for more efficient  
 CC production of drug substances and vaccines.  
 XX SQ Disclosure: Page 17; 65pp; Japanese.  
 CC Query Match 100.0%; Score 10; DB 22; Length 10;  
 CC Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
 CC Matches 6; Conservative 4; Mismatches 0;  
 CC Indels 0; Gaps 0;  
 CC OY 1 CTCGACCCU 10  
 CC Db 1 CTCGACCCU 10  
 RESULT 6  
 ID AAL47265  
 ID AAL47265 standard; DNA; 10 BP.  
 AC AAL47265;  
 XX DT 30-AUG-2002 (first entry)  
 XX DE Sendai virus S sequence complement.  
 XX KW Sendai virus vector; gene therapy; antiinflammatory; inflammation;  
 KW cardiovascular system; paranyxovirus; IL-10; pulmonary fibrosis;  
 KW sclerosing peritonitis; prostatomegaly; multiple sclerosis;  
 KW neuroprotective; immunosuppressive; antidiabetic; antirheumatic;  
 KW transplant rejection; diabetes; chronic articular rheumatism;  
 KW psoriasis; inflammatory enteropathy; systemic lupus erythematosus;  
 KW iritis; granulomatous disease; chronic nephritis; scleroderma;  
 KW hysterosomyoma; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.  
 XX OS Sendai virus.  
 XX PN WO200118223-A1.  
 XX XX 15-MAR-2001.  
 XX PD 06-SEP-2000; 2000WO-JP06051.  
 XX PR 06-SEP-1999; 99JP-0252231.  
 XX PA (DNAV-) DNA VEC RES INC.  
 XX PI Nagai Y, Kato A, Hasegawa M;  
 XX DR WPI; 2002-490069/52.

RESULT 5  
 ID AAF77598  
 ID AAF77598 standard; DNA; 10 BP.  
 XX AC AAF77598;  
 XX DT 29-MAY-2001 (first entry)  
 XX DE Modified transcription initiation site Paramyxovirus related oligo #18.  
 XX KW Transcription initiation sequence; viral vector; vaccine; therapy; ds.  
 XX OS Unidentified.  
 XX DR WPI; 2002-490069/52.

XX Novel paramyxovirus vector for gene transfer to cardiovascular system,  
 PT in which expression product of gene comprised in vector is transferred  
 PT to a site different from the site of administration through the  
 PT bloodstream -  
 XX Disclosure; Page 17; 67pp; English.  
 CC The present invention relates to a paramyxovirus vector for gene transfer  
 CC to the cardiovascular system, where the expression product of a gene  
 CC comprised in the vector is transferred to a site different from the site  
 CC of administration through the bloodstream. The vector is useful for  
 CC transferring sequences such as IL-10 to the cardiovascular system, for  
 CC treating pneumonia in cystic fibrosis patients and for treating  
 CC inflammatory diseases such as pulmonary fibrosis, sclerosing peritonitis,  
 CC prostatomegaly, multiple sclerosis, post transplant rejection, diabetes,  
 CC chronic articular rheumatism, psoriasis, inflammatory enteropathy,  
 CC systemic lupus erythematosus, iritis, granulomatous disease, chronic  
 CC nephritis, Scleroderma, hystromyoma, keloid and cirrhosis. The present  
 CC sequence is a DNA fragment used to produce the vector of the invention.  
 XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 Query Match 100.0%; Score 10; DB 24; Length 10;  
 Best Local Similarity 60.0%; Pred. NO. 4 2e+03;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUDUCACCCU 10  
 OY 1 ::::::: 10  
 Db 1 CTTTCACCC 10  
 RESULT 7  
 AAJ38107  
 ID AAJ38107 standard; DNA; 10 BP.  
 XX  
 AC AAJ38107;  
 DT 15-AUG-2002 (first entry)  
 XX Angiogenesis gene containing paramyxovirus vector related oligo #1.  
 DE  
 KW Vascotropic; paramyxovirus vector; angiogenesis gene; gene therapy; FGF2;  
 KW ischaemia; virus vector; edema; tissue targeting; ds.  
 OS Unidentified.  
 XX  
 PN WO200242481-A1.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 27-NOV-2001; 2001WO-JP10323.  
 XX  
 PR 27-NOV-2000; 2000JP-0353374.  
 XX  
 PA (DNAV-) DNAVEC RES INC.  
 XX  
 PI Yonemitsu Y, Sueishi K, Fukumura M, Hou X, Hasegawa M;  
 XX  
 DR WPI; 2002-452662/48.  
 XX  
 PT Paramyxovirus vector containing angiogenesis gene FGF2 for gene therapy  
 PT treatment targeting ischemic tissue -  
 XX  
 PS Disclosure; Page 23; 94bp; Japanese.  
 XX  
 CC The invention relates to a paramyxovirus vector containing an  
 CC angiogenesis gene, which can be used for gene therapy of ischaemia in  
 CC tissues including brain, heart, lung, skeletal muscle and kidney. The  
 CC expression of the virus vector is free from edema and specific tissues  
 CC can be targeted. This polynucleotide sequence represents an artificial  
 CC oligonucleotide relating to the paramyxovirus vector containing an  
 CC angiogenesis gene FGF2 of the invention.

SQ	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
Query Match	100.0%; Score 10; DB 24; Length 10;
Best Local Similarity	60.0%; Pred. No. 4.2e+03;
Matches	Mismatches 0; Indels 0; Gaps 0;
Matches	6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY	1 CUUUCACCCU 10  :::     ;
Db	1 CTTCACCC 10
RESULT 8	
ABK48812	
ID	ABK48812 standard; DNA; 10 BP.
XX	
AC	ABK48812;
XX	
DT	15-JUL-2002 (first entry)
DE	DNA sequence #1 relating to paramyxovirus vector for gene transfer.
XX	
KW	Method for gene transfer; skeletal muscle; paramyxovirus vector;
KW	gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective;
KW	myotropic; insulin-like growth factor; IGF; ds;
XX	Unidentified.
OS	
XX	
PN	WO200231138-A1.
XX	
PD	18-APR-2002.
XX	
PF	26-SEP-2001; 2001WO-JP08372.
XX	
PR	06-OCT-2000; 2000JP-0308533.
XX	
PA	(DNAV-) DNAV-EC RES INC.
XX	
PI	Hukumura M, Shiotani A, Maeda M, Hasegawa M;
XX	
DR	WPI; 2002-340180/37.
XX	
PT	Paramyxovirus vector for transferring foreign gene e.g. insulin-like
PT	growth factor into skeletal muscle in gene therapy of neuromuscular
PT	disorders -
XX	
PS	Disclosure; Page 14; 56pp; Japanese.
XX	
CC	The present invention relates to a method for transferring a foreign
CC	gene into skeletal muscle. The method comprises administering a
CC	paramyxovirus inserted with the foreign gene. The paramyxovirus vector
CC	is useful for transferring a foreign gene e.g. insulin-like growth
CC	factor (IGF) into skeletal muscle in the gene therapy of neuromuscular
CC	disorders. Such a vector can sustain transgene expression for up to a
CC	month after injection and is safe, non-infective and does not cause
CC	tumourigenesis. The present DNA sequence of unknown function is
CC	given in the specification of the present invention.
XX	
SQ	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
Query Match	100.0%; Score 10; DB 24; Length 10;
Best Local Similarity	60.0%; Pred. No. 4.2e+03;
Matches	Mismatches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY	1 CUUUCACCCU 10  :::     ;
Db	1 CTTCACCC 10

AC ABL39904;  
 XX KW Tourette's Syndrome; attention deficit disorder; hyperactivity;  
 DT KW post-traumatic stress disorder; PCR amplification; RFLP;  
 XX KW restriction fragment length polymorphism; ss.  
 DE Sendai virus S oligonucleotide SEQ ID NO:1.  
 XX OS Synthetic.  
 KW  
 KW Sendai virus; virus vector; renal cell; paramyxovirus; gene transfer;  
 KW gene therapy; kidney; nephrotoxic; antidiabetic; diabetes; nephopathy;  
 KW chronic glomerulonephritis; glomerulosclerosis; Alport's syndrome;  
 KW tubulointerstitial nephritis; ss.  
 XX OS Parainfluenza virus.  
 XX PN WO200200264-A1.  
 XX PR 03-JAN-2002.  
 XX PF 27-JUN-2001; 2001WO-JP05513.  
 XX PR 27-JUN-2000; 2000JP-0197870.  
 XX PA (DNAV-) DNAVEC RES INC.  
 XX PI Imai E, Isaka Y, Fukumura M, Hasegawa M;  
 DR WPI; 2002-130841/17.  
 XX PS  
 PT Transferring a gene into renal cells, useful for gene therapy of a  
 PT kidney to treat e.g. chronic glomerulonephritis, comprises using a  
 PT virus vector particularly of paramyxovirus  
 XX PS Example 1; Page 38; 75pp; Japanese.  
 XX The present invention describes transferring a gene into renal cells  
 CC comprising contacting a paramyxovirus vector with the renal cells,  
 CC particularly by administration into blood vessels, especially the renal  
 CC artery or into the urethra. Also described are: (1) a paramyxovirus  
 CC vector for use in transferring a gene into renal cells; and  
 CC (2) compositions for transferring a gene into renal cells comprising  
 CC cells having the paramyxovirus vector or the vector. The method is used  
 CC for transferring a gene into renal cells. The virus is applicable in  
 CC gene therapy for the kidney to treat target diseases of e.g. chronic  
 CC glomerulonephritis, diabetes, neuropathy, glomerulosclerosis,  
 CC tubulointerstitial nephritis and Alport's syndrome. The transfer of a  
 CC gene into renal cells is with high efficiency, and after brief exposure,  
 CC the transferred gene is continuously expressed in renal cells over a  
 CC long period of time. The present sequence represents a Sendai virus  
 CC (parainfluenza virus) oligonucleotide which is used in an example from  
 XX the present invention.  
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 Query Match 100.0%; Score 10; DB 24; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CUUUCACCCU 10  
 Db 11 CTTTCACCT 2  
 RESULT 11  
 AAU18122\_C  
 ID AAU18122 standard; DNA; 11 BP.  
 XX AC AAU18122;  
 XX DT 22-AUG-1996 (first entry)  
 DE Human dopamine D2 receptor DRD2 intron 6 polymorphic site (3208T).  
 XX KW Dopamine D2 receptor; A1 allele; B1 allele; polymerase chain reaction;  
 KW PCR amplification of specific alleles; PASA; compulsive disorder;  
 KW cocaine dependence; alcoholism; genetic susceptibility; ss.  
 XX OS Homo sapiens.  
 FH Key allele 6  
 FT Location/qualifiers /\*tag= a  
 FT /note= "nucleotides 3203-3213 of DRD2 in which  
 DE there is a T at the polymorphic position  
 XX FT 3208".  
 KW Human dopamine D2 receptor; genetic susceptibility; diagnosis;  
 KW DRD2; compulsive disorder; alcoholism; cocaine dependence;  
 XX PN US5500343-A.

PD 19-MAR-1996.  
 XX  
 PF 07-FEB-1990; 90US-0477057.  
 XX  
 PT Hepburn AG, Wang C;  
 XX  
 PR 24-JUN-1992; 92US-090983.  
 XX  
 PR 07-FEB-1990; 90US-0477057.  
 XX  
 PR 23-JAN-1992; 92US-0826222.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Blum K, Noble EP, Sheridan PJ;  
 XX  
 DR WPI; 1996-171043/17.  
 XX  
 PT Detecting genetic potential susceptibility to cocaine dependence or alcoholism - by detecting human dopamine D<sub>2</sub> receptor gene A1 or B1 allele in the subject's DNA.  
 XX  
 PS Example 3; Column 45; 56pp; English.  
 XX  
 The dopamine D<sub>2</sub> receptor DRD2(ln6-3x7) haplotype is comprised of two polymorphisms that are separated by 212 bp and span the junction of the intron 6 and exon 7 sequences. The first is a T or C at position 3208 and the second polymorphism is a T or C at position 3420, providing 4 possible haplotypes. Haplotype I is characterised by T at position 3208 and C at position 3420. The Primers #3208 and #3420 specifically amplify a 241 bp fragment dopamine D<sub>2</sub> receptor haplotype I which is associated with alcoholism. The primers are used in a claimed method for detecting generic potential susceptibility to alcoholism in human subjects. In particular, amplification is carried out using the PASA technique (i.e. PCR Amplification of Specific Alleles). In related methods, generic potential susceptibility to cocaine dependence can be detected by amplifying human dopamine D<sub>2</sub> receptor A1 and B1 alleles (primers not specified).  
 XX  
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
 XX  
 Query Match 100 0%; Score 10; DB 17; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CUUUCACCCU 10  
 DB 11 CTTTCACCT 2  
 XX  
 RESULT 12  
 AAX14846/C  
 ID AAX14846 standard; DNA; 12 BP.  
 AC AAX14846;  
 XX  
 DT 24-MAR-1999 (first entry)  
 XX  
 DE Triple helix forming nucleotides 394-395 of 23S rRNA gene.  
 XX  
 KW Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.  
 XX  
 OS Leptospira interrogans.  
 PN US5861244-A.  
 XX  
 PD 19-JAN-1999.  
 XX  
 PF 22-DEC-1993; 93US-0173489.  
 XX  
 PR 22-DEC-1993; 93US-0173489.  
 XX  
 PR 29-OCT-1992; 92US-0968436.  
 XX  
 PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
 XX  
 PT Assay of genetic sequences based on triplex formation from double stranded analyte - and Hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.  
 PT  
 PS Disclosure; Columns 21-22; 168pp; English.  
 XX  
 CC The present sequence represents a potential triple-helix forming region.  
 CC It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus.  
 CC  
 CC Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 other;  
 XX  
 SQ Query Match 100 0%; Score 10; DB 20; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CUUUCACCCU 10  
 DB 12 CTTTCACCT 3  
 XX  
 RESULT 13  
 ABF08726/C  
 ID ABF08726 standard; DNA; 13 BP.  
 AC ABF08726;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 108723 for detecting SNP TSC0027206.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; primer; ss; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic; Homo sapiens.  
 XX  
 PN WO200177394-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-1B00713.  
 XX  
 PR 07-APR-2000; 2000DE-1019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PT Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -  
 XX  
 PS Claim 1; SEQ ID 108723; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp://wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03; Indels 0; Gaps 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
|:::||||:  
Db 13 CTTTCACCC 4

RESULT 14

ABF08727

ABF08727 standard; DNA; 13 BP.

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03; Indels 0; Gaps 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
|:::||||:  
Db 13 CTTTCACCC 10

RESULT 15

ABH24716/C

ABH24716 standard; DNA; 13 BP.

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03; Indels 0; Gaps 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
|:::||||:  
Db 13 CTTTCACCC 10

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp://wipo.int/pub/published\_pct\_sequences.

XX Search completed: March 19, 2003, 00:07:18  
Job time : 168 secs

Wed Mar 19 09:04:45 2003

us-09-702-498a-33-mod.rng

GenCore version 5.1.4.p5\_4578  
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:00:11 ; Search time 37 Seconds  
 (without alignments)  
 82.886 Million cell updates/sec

Title: US-09-702-498A-33-MOD  
 Perfect score: 100.0 ; Gapext: 1.0  
 Sequence: CuuuCACCCu 10

Scoring table: IDENTITY\_NUC  
 Gapgap 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : issued Patents\_NA.\*

1: /cgn2\_6/podata/1/ina/5A.COMB.seq;\*  
 2: /cgn2\_6/podata/1/ina/5B.COMB.seq;\*  
 3: /cgn2\_6/podata/1/ina/6A.COMB.seq;\*  
 4: /cgn2\_6/podata/1/ina/6B.COMB.seq;\*  
 5: /cgn2\_6/podata/1/ina/pcruS.COMB.seq;\*  
 6: /cgn2\_6/podata/1/ina/backfile1.seq;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	10	100.0	11 1 US-07-909-383-1	Sequence 1, Appli
c 2	10	100.0	12 2 US-08-173-489C-233	Sequence 233, App
c 3	10	100.0	19 3 US-08-777-296A-95	Sequence 95, Appli
c 4	10	100.0	19 4 US-08-326-186B-95	Sequence 95, Appli
c 5	10	100.0	22 3 US-08-777-266A-94	Sequence 94, Appli
c 6	10	100.0	22 4 US-08-326-186B-94	Sequence 94, Appli
c 7	10	100.0	23 1 US-07-952-442-7	Sequence 7, Appli
c 8	10	100.0	23 1 US-08-269-766-7	Sequence 7, Appli
c 9	10	100.0	23 1 US-08-319-545-7	Sequence 7, Appli
c 10	10	100.0	23 2 US-08-092-988-7	Sequence 7, Appli
c 11	10	100.0	23 3 US-08-106-216-7	Sequence 7, Appli
c 12	10	100.0	23 4 US-08-429-034-7	Sequence 7, Appli
c 13	10	100.0	24 3 US-08-777-266A-93	Sequence 93, Appli
c 14	10	100.0	24 4 US-08-326-186B-93	Sequence 93, Appli
c 15	10	100.0	24 4 US-08-697A-39	Sequence 39, Appli
c 16	10	100.0	124 4 US-08-702-525-39	Sequence 39, Appli
c 17	10	100.0	124 5 PCT-US95-02576-39	Sequence 39, Appli
c 18	10	100.0	33 3 US-08-009-913-15	Sequence 31, Appli
c 19	10	100.0	377 2 US-08-702-652-40	Sequence 40, Appli
c 20	10	100.0	377 6 516853-1	Patent No. 5168053
c 21	10	100.0	397 2 US-08-636-597-2	Sequence 2, Appli
c 22	10	100.0	397 4 US-09-232-063-2	Sequence 2, Appli
c 23	10	100.0	438 4 US-09-228-986-56	Sequence 56, Appli
c 24	10	100.0	440 4 US-09-397-787-321	Sequence 321, Appli
c 25	10	100.0	584 4 US-09-328-111-83	Sequence 83, Appli
c 26	10	100.0	616 4 US-09-328-111-574	Sequence 574, Appli
c 27	10	100.0	650 4 US-09-328-111-189	Sequence 189, Appli

RESULT 1  
 US-07-909-383-1/c  
 ; Sequence 1, Application US/07909383  
 ; Patent No. 5500343

; GENERAL INFORMATION:

; APPLICANT: BLUM, KENNETH  
 ; APPLICANT: NOBLE, E.P.  
 ; APPLICANT: SHERIDAN, P.J.  
 ; TITLE OF INVENTION: AMELIC ASSOCIATION OF THE HUMAN  
 ; TITLE OF INVENTION: DOPAMINE (D2) RECEPTOR GENE IN  
 ; TITLE OF INVENTION: COMPELUSIVE DISORDERS  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE  
 ; STREET: P.O. BOX 4433  
 ; CITY: HOUSTON  
 ; STATE: TEXAS  
 ; COUNTRY: USA  
 ; ZIP: 77210

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/909, 383  
 FILING DATE: 19920624  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HODGINS, DANIEL S.  
 REGISTRATION NUMBER: 31,026  
 REFERENCE/DOCKET NUMBER: UPTSK:187  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 512-320-7200  
 TELEFAX: 512-474-7577  
 TELEX: NOT APPLICABLE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 base Pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 ; US-07-909-383-1

Query Match 100.0%; Score 10; DB 1; Length 11;  
 Best local similarity 60.0%; Pred. No. 6e-02;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cuuuCACCCu 10  
 |::::::::::|

Db 11 CTTTACCCCT 2

RESULT 2

US-08-173-489C-233/C

Sequence 233, Application US/08173489C

Patent No. 5861244

GENERAL INFORMATION:

APPLICANT: WANG, C. -G.

APPLICANT: HEPBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA

TITLE OF INVENTION: TRIPLE-STRAND FORMATION

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: 510 EAST 73RD STREET,

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10021.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch, 1.44MB storage

COMPUTER: IBM PC/XI/AT

OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordperfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 22 DEC 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATTORNEY/AGENT INFORMATION:

NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179

REFERENCE/DOCKET NUMBER: U9518-6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (attorney) (212) 708-1880

TELEFAX: (attorney) (212) 246-8959

INFORMATION FOR SEQ ID NO: 233:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: U9518-6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

RESULT 3

US-08-777-266A-95

Sequence 95, Application US/08777266A

Patent No. 6077833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett

APPLICANT: Timothy A. Vickers

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Protein

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777-266A

FILING DATE: December 31, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

Query Match Best Local Similarity 60.0%; Pred. No. 6 1e+02; Length 19; Matches 6; Conservative 4; Mismatches 0; Indels 0; Caps 0;

Qy 1 cuucacccu 10

Db 7 CTTTCAACCT 16

RESULT 4

US-09-326-186B-95

Sequence 95, Application US/09326186B

Patent No. 6319906

GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank

APPLICANT: Vickers, Timothy A.

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Protein

TITLE OF INVENTION: Modulation of the Expression of B7 Protein

FILE REFERENCE: ISPH-076

CURRENT FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: 08777266

PRIOR FILING DATE: 1996-12-31

NUMBER OF SEQ ID NOS: 226

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 95

SEQ ID NO: 95

LENGTH: 19  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 ; US-09-326-186B-95

Query Match 100.0%; Score 10; DB 4; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 6. 1e+02; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUCUCACCCU 10  
 |:::|||||:  
 Db 7 CTPTCACCT 16

RESULT 5  
 US-08-777-266A-94  
 ; Sequence 94, Application US/0877726A  
 ; Patent No. 607783

GENERAL INFORMATION:  
 APPLICANT: Clarence Frank Bennett  
 APPLICANT: Timothy A. Vickers  
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins  
 NUMBER OF SEQUENCES: 125  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Law Offices of Jane Massey Licata  
 STREET: 210 Lake Drive East, Suite 201  
 CITY: Cherry Hill  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08002

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/777-266A  
 FILING DATE: December 31, 1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jane Massey Licata  
 REGISTRATION NUMBER: 32,257  
 REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (609) 779-2400  
 TELEFAX: (609) 779-8488  
 INFORMATION FOR SEQ ID NO: 94:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 ANTI-SENSE: Yes  
 US-08-777-266A-94

Query Match 100.0%; Score 10; DB 4; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 6. 1e+02; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUCUCACCCU 10  
 |:::|||||:  
 Db 7 CTPTCACCT 16

RESULT 5  
 US-08-777-266A-94  
 ; Sequence 94, Application US/0877726A  
 ; Patent No. 607783

GENERAL INFORMATION:  
 APPLICANT: Clarence Frank Bennett  
 APPLICANT: Timothy A. Vickers  
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins  
 NUMBER OF SEQUENCES: 125  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Law Offices of Jane Massey Licata  
 STREET: 210 Lake Drive East, Suite 201  
 CITY: Cherry Hill  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08002

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/777-266A  
 FILING DATE: December 31, 1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jane Massey Licata  
 REGISTRATION NUMBER: 32,257  
 REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (609) 779-2400  
 TELEFAX: (609) 779-8488  
 INFORMATION FOR SEQ ID NO: 94:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 ANTI-SENSE: Yes  
 US-08-777-266A-94

Query Match 100.0%; Score 10; DB 4; Length 22;  
 Best Local Similarity 60.0%; Pred. No. 6. 2e+02; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUCUCACCCU 10  
 |:::|||||:  
 Db 7 CTPTCACCT 16

RESULT 7  
 US-07-952-442-7  
 ; Sequence 7, Application US/07952442  
 ; Patent No. 5374525

GENERAL INFORMATION:  
 APPLICANT: Lalouel, Jean-Marc  
 APPLICANT: Jeunemaire, Xavier  
 APPLICANT: Lifton, Richard P.  
 APPLICANT: Soubrie, Florent  
 APPLICANT: Kotelevtsev, Youri  
 APPLICANT: Corval, Pierre  
 TITLE OF INVENTION: Angiotensinogen Gene Variants and Predisposition to Essential Hypertension  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/952,442  
 FILING DATE: 19920930  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Irene, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 19780-104502  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)

RESULT 6  
 US-09-326-186B-94  
 ; Sequence 94, Application US/09326186B

HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

RESULT 8  
 US-08-269-766-7  
 Sequence 7, Application US/08269766  
 Patent No. 559584  
 GENERAL INFORMATION:  
 APPLICANT: Lalouel, Jean-Marc  
 APPLICANT: Jeunemaire, Xavier  
 APPLICANT: Lifton, Richard P.  
 APPLICANT: Soubrier, Florent  
 APPLICANT: Kotlevtsev, Youri  
 APPLICANT: Corvol, Pierre  
 TITLE OF INVENTION: Angiotensinogen Gene Variants and  
 TITLE OF INVENTION: Predisposition to Essential Hypertension  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WordPerfect 5.1/5.2 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/119,545A  
 FILING DATE: 7-OCT-1994  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/952,442  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Innen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 19780-104502-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEX: 202-982-8300  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

RESULT 9  
 US-08-319-545A-7  
 Sequence 7, Application US/08319545A  
 Patent No. 5763168  
 GENERAL INFORMATION:  
 APPLICANT: Lalouel, Jean-Marc  
 APPLICANT: Jeunemaire, Xavier  
 APPLICANT: Lifton, Richard P.  
 APPLICANT: Soubrier, Florent  
 APPLICANT: Kotlevtsev, Youri  
 APPLICANT: Corvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WordPerfect 5.1/5.2 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/119,545A  
 FILING DATE: 7-OCT-1994  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/952,442  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Innen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 19780-104502-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEX: 202-982-8300  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

RESULT 10  
 US-09-092-988-7  
 Sequence 7, Application US/09092988  
 Patent No. 5998145  
 GENERAL INFORMATION:  
 APPLICANT: Lalouel, Jean-Marc  
 APPLICANT: Jeunemaire, Xavier  
 APPLICANT: Lifton, Richard P.  
 APPLICANT: Soubrier, Florent

QY 1 CUUUACCCU 10  
 Db 13 CTTTCACCT 22  
 QY 1 CUUUACCCU 10  
 Db 13 CTTTCACCT 22

APPLICANT: Kotelavtsev, Youri  
 APPLICANT: Corvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 TITLE OF INVENTION: to Hypertension  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1/5.2 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/092, 988  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 PRIORITY NUMBER: 08/319, 545  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28, 957  
 REFERENCE/DOCKET NUMBER: 19780-104502-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-09-092-988-7

Query Match 100.0%; Score 10; DB 2; Length 23;  
 Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
 |:::|||||:  
 Db 13 CTTTCACCC 22

RESULT 11  
 ; Sequence 7, Application US/09106216  
 ; Patent No. 615386  
 ; GENERAL INFORMATION:  
 APPLICANT: Halouel, Jean-Marc  
 APPLICANT: Jeunemaitre, Xavier  
 APPLICANT: Lofton, Richard P.  
 APPLICANT: Soubrier, Florent  
 APPLICANT: Kotelavtsev, Youri  
 APPLICANT: Corvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 TITLE OF INVENTION: to Hypertension  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1/5.2 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/429, 034  
 FILING DATE:  
 CLASSIFICATION:

APPLICANT: Kotelavtsev, Youri  
 APPLICANT: Corvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 TITLE OF INVENTION: to Hypertension  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
 STREET: 555 Thirteenth Street N.W., Suite 701-E  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1/5.2 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/106, 216  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/  
 FILING DATE: 08-TUN-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/319, 545  
 FILING DATE: 07-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/952, 545  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28, 957  
 REFERENCE/DOCKET NUMBER: 19780-104502-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-783-6040  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "primer"  
 US-09-106-216-7

Query Match 100.0%; Score 10; DB 3; Length 23;  
 Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
 |:::|||||:  
 Db 13 CTTTCACCC 22

RESULT 12  
 ; Sequence 7, Application US/09429034  
 ; Patent No. 616527  
 ; GENERAL INFORMATION:  
 APPLICANT: Halouel, Jean-Marc  
 APPLICANT: Jeunemaitre, Xavier  
 APPLICANT: Lofton, Richard P.  
 APPLICANT: Soubrier, Florent  
 APPLICANT: Kotelavtsev, Youri  
 APPLICANT: Corvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 TITLE OF INVENTION: to Hypertension  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1/5.2 Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/429, 034  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/319,545  
 FILING DATE: 7-OCT-1994  
 APPLICATION NUMBER: US 07/952,442  
 FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 10780-104502-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-982-4810  
 TELEFAX: 202-662-8300

INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TOPOLGY: linear  
 STRANDEDNESS: single  
 TYPE: nucleic acid  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-09-429-034-7

RESULT 13  
 US-08-777-266A-93  
 Sequence 93, Application US/08777266A  
 ; Patent No. 6077833

GENERAL INFORMATION:  
 APPLICANT: Clarence Frank Bennett  
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins  
 NUMBER OF SEQUENCES: 125  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Law Offices of Jane Massey Licata  
 STREET: 210 Lake Drive East, Suite 201  
 CITY: Cherry Hill  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08002

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/777-266A  
 FILING DATE: December 31, 1996  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jane Massey Licata  
 REGISTRATION NUMBER: 32,257  
 REFERENCE/DOCKET NUMBER: ISPH-0201  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (609) 779-4400  
 TELEFAX: (609) 779-8488  
 INFORMATION FOR SEQ ID NO: 93:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24

RESULT 14  
 US-09-326-186B-93  
 Sequence 93, Application US/09326186B  
 ; Patent No. 6319906

GENERAL INFORMATION:  
 APPLICANT: Bennett, Clarence Frank  
 APPLICANT: Vickers, Timothy A.  
 TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins  
 FILE REFERENCE: ISPH-0376  
 CURRENT APPLICATION NUMBER: US/09/326,186B  
 CURRENT FILING DATE: 1999-06-04  
 PRIOR APPLICATION NUMBER: 08/777,266  
 PRIOR FILING DATE: 1996-12-31  
 NUMBER OF SEQ ID NOS: 226  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 93  
 LENGTH: 24  
 TYPE: DNA  
 FEATURE: OTHER INFORMATION: Synthetic  
 ORGANISM: Artificial Sequence  
 OTHER INFORMATION: Synthetic  
 US-09-326-186B-93

RESULT 15  
 US-08-205-697A-39/C  
 Sequence 39, Application US/08205697A  
 ; Patent No. 6218510

GENERAL INFORMATION:  
 APPLICANT: Sharpe, Arlene H.  
 APPLICANT: Borriello, Francescopaulo  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules  
 NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/205,697A

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandragoras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BWT-120

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY:

MOLECULE TYPE: cDNA

LOCATION:

US-08-205-697A-39

Query Match 100.0%; Score 10; DB 4; Length 124;  
Best Local Similarity 60.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUCUCACCCU 10

Db 13 CTTTGACCCCT 4

Search completed: March 19, 2003, 01:26:21

Job time : 38 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.4\_P5\_4578  
 Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on:

March 19, 2003, 00:40:46 ; Search time 51.5 Seconds  
 (without alignments)  
 136.284 Million cell updates/sec

Title: US-09-702-498a-33-MOD

Perfect score: 10

Sequence: 1 cuuucacccu 10

Scoring table: IDENTITY\_NUC  
 Gapext 10.0 , Gapext 1.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters:

1002604

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: /cggn2_5/podata/1/pupbna/us07_PUBCOMB.seq:*
2: /cggn2_6/podata/1/pupbna/PCT05_NEWPUB.seq:*
3: /cggn2_6/podata/1/pupbna/us06_NEWPUB.seq:*
4: /cggn2_6/podata/1/pupbna/us06_PUBCOMB.seq:*
5: /cggn2_6/podata/1/pupbna/us07_NEWPUB.seq:*
6: /cggn2_6/podata/1/pupbna/PCTUS_PUBCOMB.seq:*
7: /cggn2_6/podata/1/pupbna/us08_NEWPUB.seq:*
8: /cggn2_6/podata/1/pupbna/us08_PUBCOMB.seq:*
9: /cggn2_6/podata/1/pupbna/us09_NEWPUB.seq:*
10: /cggn2_6/podata/1/pupbna/us09_PUBCOMB.seq:*
11: /cggn2_6/podata/1/pupbna/us10_NEWPUB.seq:*
12: /cggn2_6/podata/1/pupbna/us10_PUBCOMB.seq:*
13: /cggn2_6/podata/1/pupbna/us10_NEWPUB.seq:*
14: /cggn2_6/podata/1/pupbna/us10_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	10	9 US-09-966-277-63
2	10	100.0	10	9 US-09-966-930-43
3	10	100.0	10	9 US-09-966-277-34
4	10	100.0	10	9 US-09-966-277-51
5	10	100.0	21	10 US-09-970-331-21
6	10	100.0	30	9 US-09-988-115A4
7	10	100.0	47	9 US-09-966-277-43
8	10	100.0	47	9 US-09-966-277-44
9	10	100.0	47	9 US-09-966-930-43
10	100.0	63	10	9 US-09-966-930-44
11	100.0	69	10	9 US-09-971-840-2
12	100.0	69	10	9 US-09-971-840-4
13	100.0	69	10	9 US-09-972-207-2
14	100.0	69	10	9 US-09-972-207-4
15	100.0	69	10	9 US-09-972-207-8
16	100.0	72	9	9 US-09-966-277-34
17	100.0	72	9	9 US-09-966-277-52
18	100.0	72	9	9 US-09-966-930-34
19	100.0	72	9	9 US-09-966-930-34

## ALIGNMENTS

C	20	10	100.0	72	9	US-09-966-930-51	Sequence 51, Appl
C	21	10	100.0	72	9	US-09-966-930-52	Sequence 52, Appl
C	22	10	100.0	72	10	US-09-943-922-3	Sequence 3, Appl
C	23	10	100.0	74	9	US-09-966-277-31	Sequence 31, Appl
C	24	10	100.0	74	9	US-09-966-277-32	Sequence 32, Appl
C	25	10	100.0	74	9	US-09-966-930-31	Sequence 33, Appl
C	26	10	100.0	74	9	US-09-966-930-32	Sequence 32, Appl
C	27	10	100.0	80	9	US-09-966-277-18	Sequence 18, Appl
C	28	10	100.0	80	9	US-09-966-930-18	Sequence 18, Appl
C	29	10	100.0	112	10	US-09-783-590-8499	Sequence 8499, Ap
C	30	10	100.0	114	10	US-09-864-761-28324	Sequence 28324, A
C	31	10	100.0	116	10	US-09-864-761-24131	Sequence 24131, A
C	32	10	100.0	117	10	US-09-864-761-17517	Sequence 17517, A
C	33	10	100.0	124	9	US-09-962-969-39	Sequence 39, Appl
C	34	10	100.0	124	10	US-09-837-867A-39	Sequence 39, Appl
C	35	10	100.0	130	10	US-09-764-846-334	Sequence 334, App
C	36	10	100.0	132	10	US-09-969-313-1040	Sequence 1040, Ap
C	37	10	100.0	140	10	US-09-923-874-3943	Sequence 3943, Ap
C	38	10	100.0	143	10	US-09-783-590-7779	Sequence 7779, Ap
C	39	10	100.0	148	10	US-09-864-761-23518	Sequence 23518, A
C	40	10	100.0	165	9	US-09-046-935-156	Sequence 156, App
C	41	10	100.0	165	9	US-09-878-178-156	Sequence 156, App
C	42	10	100.0	165	10	US-09-864-761-30761	Sequence 30761, A
C	43	10	100.0	165	10	US-09-878-574-11498	Sequence 11498, A
C	44	10	100.0	174	10	US-09-783-990-6678	Sequence 6678, Ap
C	45	10	100.0	180	10	US-09-983-965-2379	Sequence 2379, Ap

OY 1 cuuucacccu 10

Query Match Score: 100.0%; Score 10; Length 10;

Best Local Similarity: 60.0%; Pred. No. 1, 5e+03;

Matches: 6; Conservative: 4; Mismatches: 0; Indels: 0; Gaps: 0;

FEATURE: OTHER INFORMATION: Artificially Synthesized Sequence

SEQUENCE: US-09-966-277-63

Db      1 ::::::: 10 .  
; CTTTCACCT 10  
; ;  
; RESULT 2  
; Sequence 63, Application US/09956930  
; Publication No. US20030022276A1  
; GENERAL INFORMATION:  
;   APPLICANT: KITAZATO, Kai  
;   APPLICANT: SHU, Tsugumine  
;   APPLICANT: KUMA, Hidekazu  
;   APPLICANT: UEDA, Yasuji  
;   APPLICANT: ASAKAWA, Makoto  
;   APPLICANT: HASEGAWA, Mamoru  
;   APPLICANT: ILDA, Akihiro  
;   APPLICANT: HITOMI, Takahiro  
;   APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
; FILE REFERENCE: 50026/029001  
; CURRENT APPLICATION NUMBER: US/09/966,930  
; CURRENT FILING DATE: 2001-09-27  
; PRIORITY APPLICATION NUMBER: PCT/JP00/03194  
; PRIORITY FILING DATE: 2000-05-18  
; PRIORITY APPLICATION NUMBER: JP 2001/283451  
; PRIORITY FILING DATE: 2001-09-18  
; PRIORITY APPLICATION NUMBER: JP 11/200740  
; PRIORITY FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
; US-09-966-930-63  
Query Match      100.0%; Score 10; DB 9; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CUUUCACCCU 10  
Db 1 CTTTCACCT 10  
  
RESULT 3  
US-09-823-699-1  
; Sequence 1, Application US/09823699  
; Patent No. US2003002143A1  
; GENERAL INFORMATION:  
;   APPLICANT: Kano, Munehide  
;   APPLICANT: Matano, Tetsuro  
;   APPLICANT: Kato, Atsushi  
;   APPLICANT: Nagai, Yoshiyuki  
;   APPLICANT: Hasegawa, Mamoru  
; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus  
; TITLE OF INVENTION: Vector  
; FILE REFERENCE: 5026/022002  
; CURRENT APPLICATION NUMBER: US/09/823-,699  
; CURRENT FILING DATE: 2001-03-30  
; PRIORITY APPLICATION NUMBER: US 60/193,127  
; PRIORITY FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificially synthesized sequence  
; US-09-823-699-1  
; LENGTH: 30  
; TYPE: DNA  
  
Query Match      100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CUUUCACCCU 10  
Db 1 CTTTCACCT 10  
  
RESULT 4  
US-09-972-331-21/c  
; Sequence 21, Application US/09972331  
; Patent No. US20020091083A1  
; GENERAL INFORMATION:  
;   APPLICANT: HIGASHI, KIYOSHI  
;   APPLICANT: KOMATSU, KENGO  
; TITLE OF INVENTION: DNA-BINDING PROTEIN YB-1-CONTAINING  
; FILE REFERENCE: 7372/72170  
; CURRENT APPLICATION NUMBER: US/09/972,331  
; CURRENT FILING DATE: 2001-12-28  
; PRIORITY APPLICATION NUMBER: JP 2000/310624  
; PRIORITY FILING DATE: 2000-10-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: DESIGNED OLIGOONUCLEOTIDE PRIMER TO SYNTHESIZE  
; US-09-972-331-21  
Query Match      100.0%; Score 10; DB 10; Length 21;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CUUUCACCCU 10  
Db 11 CTTTCACCT 2  
  
RESULT 5  
US-09-988-115A-43  
; Sequence 43, Application US/09988115A  
; Publication No. US2003003734A1  
; GENERAL INFORMATION:  
;   APPLICANT: Robl, James M.  
;   APPLICANT: Goldsby, Richard A.  
;   APPLICANT: Ferguson, Stacy E.  
;   APPLICANT: Kuroiwa, Yoshima  
;   APPLICANT: Tonizuka, Kazuma  
;   APPLICANT: Ishida, Isao  
; TITLE OF INVENTION: Expression of Xenogenous (Human) Immunoglobulins in Cloned, Transgenic Ungulates  
; FILE REFERENCE: 5019/008003  
; CURRENT APPLICATION NUMBER: US/09/988-115A  
; CURRENT FILING DATE: 2002-08-09  
; PRIORITY APPLICATION NUMBER: US 60/311,625  
; PRIORITY FILING DATE: 2001-08-09  
; PRIORITY APPLICATION NUMBER: US 60/256,458  
; PRIORITY FILING DATE: 2000-12-20  
; PRIORITY APPLICATION NUMBER: US 09/714,185  
; PRIORITY FILING DATE: 2000-11-17  
; PRIORITY APPLICATION NUMBER: US 60/166,410  
; PRIORITY FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 30  
; TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Synthetic Primer

US-09-988-115A-43

Query Match Score 10; DB 9; Length 30;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03; Mismatches 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
Db 11 CTTTCACCCCT 20

RESULT 6

US-09-966-277-43/c

; Sequence 43, Application US/09966277  
; Patent No. US20020169306A1

GENERAL INFORMATION:

APPLICANT: KITAZATO, Kai  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: TIDDA, Akihiro  
APPLICANT: HIRATA, Takahiro  
APPLICANT: TOKUSUMI, Tsuyoshi  
APPLICANT: INOUE, Makoto

TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS

TYPE: VECTOR

FILE REFERENCE: 50026/028001

CURRENT APPLICATION NUMBER: US/09/966, 277

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: PCT/JP00/03195

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 11/200739

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 43

SEQ ID NO 43

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-277-44

Query Match Score 10; DB 9; Length 47;  
Best Local Similarity 60.0%; Pred. No. 1.8e+03; Mismatches 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
Db 35 CTTTCACCCCT 44

RESULT 8

US-09-966-930-43/c

; Sequence 43, Application US/09966930

GENERAL INFORMATION:

Publication No. US20030022376A1

APPLICANT: KITAZATO, Kai  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: TIDDA, Akihiro  
APPLICANT: HIRATA, Takahiro  
APPLICANT: INOUE, Makoto

TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP

FILE REFERENCE: 50026/029001

CURRENT APPLICATION NUMBER: US/09/966, 930

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: PCT/JP00/03194

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 2001/283451

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: JP 11/200740

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 43

SEQ ID NO 43

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-930-43

Query Match Score 10; DB 9; Length 47;  
Best Local Similarity 60.0%; Pred. No. 1.8e+03; Mismatches 0;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
Db 13 CTTTCACCCCT 44

RESULT 7

US-09-966-277-44

; Sequence 44, Application US/09966277  
; Patent No. US20020169306A1

GENERAL INFORMATION:

APPLICANT: KITAZATO, Kai  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihiro  
APPLICANT: TOKTOU, Fumino

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Artificially Synthesized Sequence

Db 13 CTTTCACCT 4

Qy	1 CUUUCACCCU 10	Db	17 CTTTCACCT 26
RESULT 9		RESULT 11	
; Sequence 44, Application US/09966930		; Sequence 2, Application US/09471840	
; Publication No. US20030022376A1		; Patent No. US2003008106A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: KITAZATO, Kai		; APPLICANT: NAGAI, Yoshiyuki	
; APPLICANT: SHU, Tsugumine		; APPLICANT: KATO, Atsushi	
; APPLICANT: UEDA, Yasuji		; APPLICANT: MURAI, Fukashi	
; APPLICANT: KUMA, Hidekazu		; APPLICANT: ASAKAWA, Makoto	
; APPLICANT: ASAKAWA, Makoto		; APPLICANT: SAKATA, Tsuneki	
; APPLICANT: HASEGAWA, Mamoru		; APPLICANT: SHIODA, Tatsuo	
; APPLICANT: TIDE, Akihiro		; TITLE OF INVENTION: Autonomous Strand RNA Viral Vector Having	
; APPLICANT: HIRATA, Takahiro		; FILE REFERENCE: 50026/004002	
; APPLICANT: INOUE, Makoto		; CURRENT APPLICATION NUMBER: US/09/471,840	
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP		; CURRENT FILING DATE: 1999-12-23	
; FILE REFERENCE: 50026/029001		; EARLIER APPLICATION NUMBER: JP HEI 7-308315	
; CURRENT APPLICATION NUMBER: US/09/966,930		; EARLIER FILING DATE: 1995-10-31	
; CURRENT FILING DATE: 2001-09-27		; EARLIER APPLICATION NUMBER: PCT/JPP96/03068	
; PRIOR APPLICATION NUMBER: PCT/JP00/03194		; EARLIER FILING DATE: 1995-10-22	
; PRIOR FILING DATE: 2000-05-18		; EARLIER APPLICATION NUMBER: 03/070,938	
; PRIOR APPLICATION NUMBER: JP 2001/283451		; EARLIER FILING DATE: 1998-04-30	
; PRIOR FILING DATE: 2001-09-18		; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.	
; PRIOR FILING DATE: 1999-05-18		; SOFTARE: FastSEQ for Windows Version 4.0	
; SOFTWARE: FastSEQ for Windows Version 4.0		; LENGTH: 69	
; SEQ ID NO 44		; TYPE: DNA	
; LENGTH: 47		; ORGANISM: Human Immunodeficiency Virus	
; TYPE: DNA		; FEATURE:	
; ORGANISM: Artificial Sequence		; NAME/KEY: variation	
; FEATURE:		; LOCATION: (35)..(35)	
; OTHER INFORMATION: Artificially Synthesized Sequence		; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.	
US-09-966-930-44		US-09-471-840-2	
Db 35 CTTTCACCT 44		Db 2	
RESULT 10		RESULT 11	
; Sequence 10, Application US/09823699		; Sequence 2, Application US/09471840	
; Patent No. US20020003143A1		; Patent No. US2003008106A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Kano, Munehide		; APPLICANT: NAGAI, Yoshiyuki	
; APPLICANT: Matano, Tetsuro		; APPLICANT: KATO, Atsushi	
; APPLICANT: Kato, Atsushi		; APPLICANT: MURAI, Fukashi	
; APPLICANT: Nada, Yoshiyuki		; APPLICANT: ASAKAWA, Makoto	
; APPLICANT: Hasegawa, Mamoru		; APPLICANT: SAKATA, Tsuneki	
; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus		; APPLICANT: SHIODA, Tatsuo	
; TITLE OF INVENTION: Vector		; TITLE OF INVENTION: Autonomous Strand RNA Viral Vector Having	
; FILE REFERENCE: 50026/022002		; FILE REFERENCE: 50026/004002	
; CURRENT APPLICATION NUMBER: US/09/823,699		; CURRENT APPLICATION NUMBER: US/09/471,840	
; CURRENT FILING DATE: 2001-03-30		; CURRENT FILING DATE: 1999-12-23	
; PRIOR APPLICATION NUMBER: US 60/193,127		; EARLIER APPLICATION NUMBER: JP HEI 7-308315	
; PRIOR FILING DATE: 2000-03-30		; EARLIER FILING DATE: 1995-10-31	
; NUMBER OF SEQ ID NOS: 18		; EARLIER APPLICATION NUMBER: PCT/JPP96/03068	
; SOFTWARE: FastSEQ for Windows Version 4.0		; EARLIER FILING DATE: 1995-10-22	
; SEQ ID NO 10		; EARLIER APPLICATION NUMBER: 03/070,938	
; LENGTH: 63		; EARLIER FILING DATE: 1998-04-30	
; TYPE: DNA		; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.	
; ORGANISM: Artificial Sequence		; SOFTARE: FastSEQ for Windows Version 4.0	
; FEATURE:		; LENGTH: 69	
; OTHER INFORMATION: artificially synthesized sequence		; TYPE: DNA	
US-09-823-699-10		; ORGANISM: Human Immunodeficiency Virus	
Db 1 CUUUCACCCU 10		; FEATURE:	
Qy 1 CUUUCACCCU 10		; NAME/KEY: variation	
Db 17 CTTTCACCT 26		; LOCATION: (35)..(35)	
RESULT 12		; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.	
US-09-471-840-4		; SOFTARE: FastSEQ for Windows Version 4.0	
; Sequence 4, Application US/09471840		; LENGTH: 69	
; Patent No. US200200081706A1		; TYPE: DNA	
; GENERAL INFORMATION:		; ORGANISM: Human Immunodeficiency Virus	
; APPLICANT: NAGAI, Yoshiyuki		; FEATURE:	
; APPLICANT: KATO, Atsushi		; NAME/KEY: variation	
; APPLICANT: MURAI, Fukashi		; LOCATION: (35)..(35)	
; APPLICANT: ASAKAWA, Makoto		; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.	
; APPLICANT: SAKATA, Tsuneki		; SOFTARE: FastSEQ for Windows Version 4.0	
; APPLICANT: HASEGAWA, Mamoru		; LENGTH: 69	
; APPLICANT: SHIODA, Tatsuo		; TYPE: DNA	
; TITLE OF INVENTION: Autonomous Strand RNA Viral Vector Having		; ORGANISM: Human Immunodeficiency Virus	
; FILE REFERENCE: 50026/004002		; FEATURE:	
; CURRENT APPLICATION NUMBER: US/09/471,840		; NAME/KEY: variation	
; CURRENT FILING DATE: 1999-12-23		; LOCATION: (35)..(35)	
; EARLIER APPLICATION NUMBER: JP HEI 7-308315		; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.	
; EARLIER FILING DATE: 1995-10-31		; SOFTARE: FastSEQ for Windows Version 4.0	
; EARLIER APPLICATION NUMBER: PCT/JPP96/03068		; LENGTH: 69	

; EARLIER FILING DATE: 1995-10-22  
; EARLIER APPLICATION NUMBER: 09/070,938  
; EARLIER FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 69  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemical synthesis  
; US-09-471-840-4

Query Match 100.0%; Score 10; DB 10; Length 69;  
Best Local Similarity 60.0%; Pred. No. 1.9e+03;  
Matches 6; Conservative 4; Mismatches 0;  
Indels 0; Gaps 0;

Qy 1 CUUUCACCCU 10  
Db 16 CTTTCACCT 25

RESULT 13

US-09-728-207-2  
Sequence 2, Application US/09728207  
Patent No. US20020096576A1

GENERAL INFORMATION:

APPLICANT: NAGAI, Yoshiyuki  
APPLICANT: KATO, Atsushi  
APPLICANT: MORAI, Fukashi  
APPLICANT: SAKATA, Tsuneaki  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: SHIODA, Tatsuo

FILE REFERENCE: Recombinant Sendai Virus  
CURRENT APPLICATION NUMBER: US/09/728,207  
CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: US/09/071,591  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: JP HEI 7-285417  
PRIOR FILING DATE: 1995-11-01  
PRIOR APPLICATION NUMBER: PCT/JP96/03069  
PRIOR FILING DATE: 1996-10-22

NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 2

LENGTH: 69  
NAME/KEY: variation  
LOCATION: (35)::(35)  
OTHER INFORMATION: v at 35 is a, c, or g, not t or u.

US-09-728-207-2

RESULT 15

US-09-070-938-2  
Sequence 2, Application US/09070938  
Patent No. US20020100066A1

GENERAL INFORMATION:

APPLICANT: Nagai, Yoshiyuki  
APPLICANT: Kato, Atsushi  
APPLICANT: Murai, Fukashi  
APPLICANT: Asakawa, Makoto  
APPLICANT: Sakata, Tsuneaki  
APPLICANT: Hasegawa, Mamoru  
APPLICANT: Shioda, Tatsuo

FILE REFERENCE: Negative Strand RNA Viral  
TITLE OF INVENTION: Vector Having Autonomous Replication Capability  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,938  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-308315  
FILING DATE: 31-OCT-1995  
APPLICATION NUMBER: JP96/03068  
FILING DATE: 22-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 5026/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200

RESULT 14

US-09-728-207-4  
Sequence 4, Application US/09728207  
Patent No. US20020098576A1  
GENERAL INFORMATION:  
APPLICANT: NAGAI, Yoshiyuki  
APPLICANT: KATO, Atsushi  
APPLICANT: MURAI, Fukashi  
APPLICANT: SAKATA, Tsuneaki

TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
US-09-070-938-2

Query Match 100.0%; Score 10; DB 10; Length 69;  
Best Local Similarity 60.0%; Pred. No. 1.9e+03;  
Matches 6; Conservative 4; Mismatches 0;  
Indels 0; Gaps 0;

QY 1 CUUUGACCCU 10  
|:::|||||:  
Db 17 CTTTGACCC 26

Search completed: March 19, 2003, 02:47:57  
Job time : 51.5 secs

Copyright (c) 1993 - 2003 CompuGen Ltd.

Om nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:53:50 : search time 1320.5 seconds  
 (without alignments)  
 122.647 Million cell updates/sec

Scoring table:	us-09-702-498A-33-MOD
Perfect score:	1 cuucuACCCu 10
Sequence:	
Searched:	16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters:	32308132
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
Maximum Match 100%	
Listing first 45 summaries	
database :	
EST:*	
1: em_estha:*	
2: em_esthum:*	
3: em_estin:*	
4: em_estmu:*	
5: em_estov:*	
6: em_estpl:*	
7: em_estro:*	
8: em_htc:*	
9: em_estf:*	
10: gb_estc:*	
11: gb_htc:*	
12: gb_est3:*	
13: gb_estt:*	
14: gb_est5:*	
15: em_estfun:*	
16: em_lestom:*	
17: gb_gss:*	
18: em_gss_hum:*	
19: em_gss_inv:*	
20: em_gss_pln:*	
21: em_gss_vrt:*	
22: em_gss_fun:*	
23: em_gss_mam:*	
24: em_gss_mus:*	
25: em_gss_other:*	
26: em_gss_pro:*	
27: em_gss_rnd:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	28	TAA285H02Q
2	10	100.0	38	A1485473 T. brucei
3	10	100.0	43	A2332275 1M060M11
4	10	100.0	67	ALJ754476 Arabidops
5	10	100.0	68	A2805524 2M0066P22
6	10	100.0	72	BE138421 XR74904.x
			BT1783611 kh35e05.	

**ALIGNMENTS**

RESULT	1	TA285H02Q	TA285H02Q	LOCUS	28 bp DNA clone 285h02, reverse sequence,	DEFINITION	T. brucei sheared genomic DNA clone 285h02, reverse sequence, genomic survey sequence.
1	1	AL085473	AL085473.1	VERSION	GI:11853036	KEYWORDS	GSS.
2	1	AL085473	AL085473.1	SOURCE	TRYPANOSOMA BRUCEI	ORGANISM	Trypanosoma brucei.
3	1	AL085473	AL085473.1	REFERENCE	1 (bases 1 to 28)	AUTHORS	Hajil,N., Bowman,S., Leonard,N.J., Doggett,J., Atkin,R.,' Hou,L., Chillingworth,C., Ormond,D., Harris,B., El-Bayed,N., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
4	1	AL085473	AL085473.1	TITLE		JOURNAL	
5	1	AL085473	AL085473.1	COMMENT	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Direct Submission	ROCKVILLE, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRYP92/4 Guraat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Insert Sequencing: A Practical Approach, eds. M. Vaudin and R.	

Barrell, Oxford University Press, 1999).

Email: nelsayed@tgtr.org  
Details of *T. brucei* sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).

## FEATURES

source

1..28

/organism="Trypanosoma brucei"

/db\_xref="taxon:5691"

/clone="85h02"

BASE COUNT

5

a

10

c

2

g

11

t



DEFINITION	Kh35e05.y1 Ascaris suum male head pAMP1 v2 Chiapelli McCarter	ACCESSION	AZ781553
ORGANISM	Ascaris suum	VERSION	AZ781553.1
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea	KEYWORDS	GSS.
LOCUS	Ascaridida; Ascaris.	VERSION	house mouse.
DEFINITION	1 (bases 1 to 72)	SOURCE	Mus musculus
KEYWORDS	(bases 1 to 72)	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
EST.		REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SOURCE		AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
JOURNAL	Ascaris suum	COMMENT	Islam,H., Longacre,S., Mahmoud,M., Meinen,E., Pedersen,T., Reilly,
COMMENT		CONTACT	M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
TITLE	pig roundworm.	CONTACT	and Wright,D., Weiss,R.
JOURNAL		TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT		JOURNAL	Plasmid inserts
Unpublished (1999)		COMMENT	Unpublished (2000)
Contact: McCarter JP		CONTACT	Contract: Robert B. Weiss
The Washington Univ. Nematode EST Project, 1999		CONTACT	University of Utah Genome Center
Washington University School of Medicine		CONTACT	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		CONTACT	84112, USA
Tel: 314 286 1800		CONTACT	Tel: 801 585 5606
Fax: 314 286 1810		CONTACT	Fax: 801 585 7177
Email: est@wustl.edu		FEATURES	Seq primer: CGTGTAAACGAGCCAGT
The library was constructed by Brandi Chiapelli and Dr. James		source	Class: plasmid ends
McCarter at Washington University, St. Louis. The cDNA was made by			Insert Length: 10000 Std Error: 0.00
using Dynabead oligo-dT priming (Dynal). PCR based library using a			Plate: 0021 Row: I Col: 03
modified protocol from the SMART PCR cDNA Synthesis Kit from			Row: 0021 Column: 03
Clontech. Directionally cloned into the UDG sites of pAMP1.			Seq primer: CGTGTAAACGAGCCAGT
Dissected nematode tissues were provided by Dr. Alan Scott			Class: plasmid ends
(ascott@hsph.edu) of the School of Public Hygiene and Public Health			High quality sequence stop: 72.
at John Hopkins University in Baltimore, MD.			Location/qualifiers
Seq Primer: -40RP from Gibco			1. .72
High quality sequence stop: 58.			/organism="Mus musculus"
location/Qualifiers			/strain="C57BL/6J"
1. .72			/db_xref="taxon:10090"
/organism="Ascaris suum"			/clone="UUCG2MM021103"
/db_xref="taxon:6253"			/clone.lib="Ascaris suum male head pAMP1 v2 Chiapelli
/clone.lib="Ascaris suum male head pAMP1 v2 Chiapelli			/sex="Male,"
McCarter"			/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/sex="Male"			/note="Vector: PWD42nv; Purified genomic DNA from M.
/tissue_type="Head"			musculus C57BL/6J (male)" was obtained from the Jackson
/dev_stager="Adult"			Laboratory Mouse DNA Resource
/lab_host="DH10B"			(http://www.Jax.org/Resources/documents/dnarecs/). The DNA
/note="Vector: PAMP1 (Gibco); Site_1: NotI; Site_2: SalI;			was hydrodynamically sheared by repeated passage through a
The library was constructed by Brandi Chiapelli and Dr.			0.005 1inch orifice at constant velocity. The sheared DNA
James McCarter at Washington University, St. Louis. The			was blunt end-repaired with T4 DNA polymerase and T4
cDNA was made by using Dynabead oligo-dT priming (Dynal).			polynucleotide kinase. Adaptor oligonucleotides were
PCR based library using a modified protocol from the SMART			ligated to the blunt ends in high molar excess. The
PCR cDNA Synthesis Kit from Clontech. Directionally cloned			adapted DNA was purified and size-selected for a 9.5 to
into the UDG sites of PAMP1. Dissected nematode tissues			10.5 kb range using preparative agarose gel
were provided by Dr. Alan Scott (ascott@hsph.edu) of the			electrophoresis. Vector DNA was prepared from a derivative
School of Public Hygiene and Public Health at John Hopkins			of pMD42 (g114j32114gb.MP129072.1), a copy-number
University in Baltimore, MD."			inducible derivative of Plasmid R1. The vector was ligated
ORIGIN			with adaptors complementary to the insert adaptors and
BASE COUNT	10 a 22 c		purified. The sheared, adapted mouse DNA was annealed to
Query Match	100.0%		adapted vector DNA, and transformed into
Best Local Similarity	60.0%		chemically competent E. coli XL10-Gold (Stratagene) cells
Matches	6; Conservative		and selected for ampicillin resistance.
Qy	1 CUUCACCCU 10		5 a 26 c 3 g 38 t
Db	26 CTTTCACCT 35		
RESULT 7			
AZ781553	AZ781553	72 bp DNA	linear GSS 16-FEB-2001
LOCUS	2M002103F	Mouse 10kb plasmid UGGC1M library	Mus musculus genomic
DEFINITION	clone UGGC1M002103 F, DNA sequence.		
RESULT 8			
B36161/C	B36161	73 bp DNA	linear GSS 17-OCT-1997
LOCUS	HS-U038-A1-ELL-MF-ab1 CIR Human Genomic Sperm Library C Homo		
DEFINITION	sapiens genomic clone Plate=CT 820 Col=21 Row=1, DNA sequence.		

		source	1. .80
ACCESSION	B30161	/organism="Takifugu rubripes"	
VERSION	B36161.1	/db_xref="taxon:31033"	
KEYWORDS	GSS.	/clone="152F5ag3"	
SOURCE	Homo sapiens	/clone_11b="cosmid 152R05"	
REFERENCE	1 (bases 1 to 73)	BASE COUNT	7 a 22 c 13 g 35 t
AUTHORS	Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.	ORIGIN	3 others
TITLE	Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors	Qy	1 CUUCACCCU 10
JOURNAL	Unpublished (1997)	Db	39 CTTTCACCCCT 48
COMMENT	Contact: Mahairas GG, Zackrone KD, Hood L Seattle, WA 98195, USA Tel: (206) 616-8744 Fax: (206) 685-7701 Email: kackron@u.washington.edu	RESULT 10	B1550671
	Sequence Tagged Connector	LOCUS	B1550671 84 bp mRNA linear EST 05-SEP-2001
	Plate: CT 820 row: I column: 21	DEFINITION	Best Local Similarity 60.0%; Score 10; DB 17; Length 80;
	Class: BAC ends	BASE COUNT	Matches 6; Conservative 4; Mismatches 0; indels 0; Gaps 0;
	High quality sequence stop: 73.	VERSION	
FEATURES	Location/Qualifiers	KEYWORDS	
SOURCE	1. .73	ORGANISM	
	/organism="Homo sapiens"	REFERENCE	
	/db_xref="taxon:9606"	AUTHORS	1 (bases 1 to 84)
	/clone="Plate=CT 820 Col=21 Row=I"	TITLE	NIH-MGC http://mgc.ncbi.nih.gov/
	/clone_11b="CIT Human Genomic Sperm Library C"	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
BASE COUNT	21 a 14 c 21 g 16 t 1 others	COMMENT	Contact: Robert Straubberg, Ph.D. Email: cgaps-r@mail.nih.gov
ORIGIN			Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Yoshiaki and Piero Carninci (RIKEN) DNA Sequencing by: Incyte Genetics, Inc. Clone distribution by: Incyte Genetics, Inc. found through the T.M.A.G.E. Consortium information can be found at: http://image.llnl.gov plate: LLAM11695 row: 1 column: 12
Query Match	100.0%; Score 10; DB 17; Length 73;	FEATURES	High quality sequence stop: 84.
Best Local Similarity	60.0%; Pred. No. 9.6e+04;	SOURCE	Location/Qualifiers
Matches	6; Conservative 4; Mismatches 0;	1. .84	
QY	1 CUUCACCCU 10	source	
Db	28 CTTTCACCCCT 48	/organism="Homo sapiens"	
RESULT 9		/db_xref="taxon:9606"	
FR0032825		/clone="IMAGE:5275475"	
LOCUS	FR0032825	/clone_11b="NIH_MGC_95"	
DEFINITION	Fugu rubripes GSS sequence, clone 152F5ag3, genomic survey	/tissue_type="hippocampus"	
ACCESSION	AL029193	/lab_host="DH10B"	
VERSION	AL029193.1	/note="Organ: brain; Vector: pBluescript PTR (modified pBluescript KS+); Site.1: BamHI; Site.2: SalI-XbaI (gtcgag	
KEYWORDS	GI:3271307	; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NICHD, National Institutes of Health). Note: this is a NIH-MGC library."	
SOURCE			
ORGANISM			
REFERENCE	Takifugu rubripes.		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.		
TITLE	Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.		
JOURNAL	Submitted (09 JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biohep@hmp.mrc.ac.uk		
COMMENT	Direct Submission	BASE COUNT	19 a 19 c 30 g 16 t
V_TYPE	Bluescript II KS	ORIGIN	
PRIMER	phagemid	Qy	1 CUUCACCCU 10
DESCR:	One pass dye-terminator sequencing of cosmid cloned genomic sequence.	Db	21 CTTTCACCCCT 30
FEATURES	Location/Qualifiers		

RESULT 11  
 BH405910 BH405910 88 bp DNA linear GSS 19-APR-2002  
 LOCUS BH405910-105F8-SP6E RPCI-23 Mus musculus genomic clone RPCI-23-105F8  
 DEFINITION , DNA sequence.  
 ACCESSION BH405910  
 VERSION BH405910.1 GI:17460796  
 KEYWORDS GSS,  
 house mouse.  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 (bases 1 to 88)  
 AUTHORS Young, J.M., Friedman, C., Williams, E.M., Ross, J.A., Tonnes-Priddy, L.  
 and Trask, B.J.  
 TITLE Different evolutionary processes shaped the mouse and human  
 olfactory receptor gene families  
 JOURNAL Hum. Mol. Genet. 11 (5), 535-546 (2002)  
 MEDLINE 21864068  
 COMMENT Contact: Young JM  
 Barbara Trask, division of Human Biology  
 Fred Hutchinson Cancer Research Center  
 1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA  
 Tel: 206 667 1471  
 Fax: 206 667 6524  
 Email: layoung@fhcrc.org  
 Young, J.M., Swartzell, S., Friedman, C., Tonnes-Priddy, L., Lane, R.P.,  
 Wallace, J.C., Mahairas, G.G., Hood, L., and Trask, B.J. End sequences  
 of mouse BACs containing olfactory receptor genes. Unpublished  
 Plate: 105 Row: F column: 8  
 Seq primer: SP6E  
 Class: BAC ends.

FEATURES source  
 Location/Qualifiers  
 1. . 88  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10990"  
 /clone="RPCI-23-105F8"  
 /clone\_lib="RPCI-23"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney/Brain; vector: pBACE3.6; Site\_1:  
 EcoRI; Site\_2: EcoRI; female C57BL/6J mouse kidney and/or  
 brain genomic DNA was isolated and partially digested  
 with a combination of EcoRI and EcoRI Methylase. Size  
 selected DNA was cloned into the pBACE3.6 vector at the  
 EcoRI sites. The ligation products were transformed into  
 DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT  
 ORIGIN 19 a 34 c 11 g 24 t

Query Match 100.0%; Score 10; DB 17; Length 88;  
 Best Local Similarity 60.0%; Pred. No. 9.9e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
 :::::::::::::  
 Db 77 CTTTCACCC 86

---

RESULT 12  
 A2659166 A2659766 93 bp DNA linear GSS 14-DEC-2000  
 LOCUS 1M037H21F Mouse 10kb plasmid UGGCLM library Mus musculus genomic  
 DEFINITION clone UGGCLM037H21 F, DNA sequence.  
 ACCESSION A2659766  
 VERSION A2659766.1 GI:11796912  
 KEYWORDS GSS,  
 house mouse.  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1  
 (bases 1 to 93)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenah, B., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A.,  
 and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL University of Utah Genome Center  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5605  
 Fax: 801 585 7177  
 Email: dwein@genetics.utah.edu  
 Insert length: 10000 Std error: 0.00  
 Plate: 0537 Row: H column: 21  
 Seq primer: CGTTGTTAACAGACGCCAGT  
 Class: Plasmid ends  
 High quality sequence stop: 93.  
 Location/Qualifiers  
 1. . 93  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10990"  
 /clone="UUGCLM037H21"  
 /clone\_lib="Mouse 10kb plasmid uggclm library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pWD42nv; Purified genomic DNA from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.Jax.org/resources/documents/dnars/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptored DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (911473211419bAF12072.1), a copy number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptored mouse DNA was annealed to  
 adaptored vector DNA and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN 17 a 30 c 20 g 26 t

Query Match 100.0%; Score 10; DB 17; Length 93;  
 Best Local Similarity 60.0%; Pred. No. 1e+05;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
 :::::::::::::  
 Db 9 CTTTCACCC 18

---

RESULT 13  
 AG101870 AG101870 93 bp DNA linear GSS 03-NOV-2001  
 LOCUS AG101870 Pan troglodytes DNA, clone: PTB-105A03.R, genomic survey sequence.  
 DEFINITION Pan troglodytes DNA, clone: PTB-105A03.R, genomic survey sequence.  
 ACCESSION AG101870  
 VERSION AG101870.1 GI:16722387  
 KEYWORDS GSS,  
 Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male  
 SOURCE BAC Library clone:PTB-105A03.R.  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE source  
 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 AUTHORS /organism="Homo sapiens"  
 Tottori,Y., Watanabe,H. and Sakaki,Y.  
 TITLE /db\_xref="taxon:9605"  
 JOURNAL /clone="IMAGE:1861992"  
 Unpublished /clone\_lib="NCI\_CGAP\_OV26"  
 /sex="female"  
 REFERENCE 2 /tissue\_type="Papillary serous carcinoma"  
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Toki,Y., Watanabe,H. and Sakaki,Y.  
 TITLE Direct Submission  
 JOURNAL /dev\_stage="adult"  
 submitted (07-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 (E-mail: chieh@riken.gsc.riken.go.jp/;  
 Tel: 81-45-503-9111; Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.

PRIMERS Sequencing: M13Rev

LIBRARY Vector : PKS145

R\_Site 1 : SacI

R\_Site 2 : SacI

FEATURES Location/Qualifiers

source 1. .93

/organism="Pan troglodytes"  
 /db\_xref="taxon:9598"  
 /clone="PRB-105A03.R"  
 /sex="male"  
 /cell\_type="lymphoblast"  
 /clone\_id="PRB Chimpanzee Male BAC Library"

BASE COUNT 11 a 34 c 8 g 34 t 6 others

ORIGIN Query Match 100.0%; Score 10; DB 17; Length 93;  
 Best Local Similarity 60.0%; Pred. No. 1e+05; Matches 6;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUCUCACCCU 10  
 ||:|||||:  
 Db 45 CTTTCACCC 54

---

RESULT 14

A1053521 AT053527 AT053527 mRNA sequence.  
 LOCUS q172a08\_x1 NCI\_CGAP\_OV26 Homo sapiens CDNA clone IMAGE:1862006 3',  
 DEFINITION mRNA sequence.  
 ACCESSION A1053527  
 VERSION A1053527.1 GI:3321314  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 97)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 JOURNAL Tumor Gene Index  
 COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-r@mail.nih.gov  
 Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 DNA Library Preparation: David B. Krizman, Ph.D.  
 CGNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the T.M.A.G.E. Consortium/LINL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40m13 fwd. ER from Amersham.

FEATURES Location/Qualifiers

source 1. .97

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1862006"  
 /clone\_id="NCI\_CGAP\_OV26"  
 /sex="female"  
 /tissue\_type="Papillary serous carcinoma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="organ: ovary; vector: PAM1; mRNA made from  
 papillary serous ovarian carcinoma; CDNA made by oligo-dT  
 priming. Directionally cloned. Size-selected on agarose  
 gel, average insert size 500 bp. Primary library,  
 non-amplified." Primary library, Primary library,  
 found through the T.M.A.G.E. Consortium/LINL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40m13 fwd. ER from Amersham.

FEATURES Location/Qualifiers

Query Match

Wed Mar 19 09:04:45 2003

us-09-702-498a-33-mod.rst

Page 8

Best Local similarity 60.0%; Pred. No. 1e+05; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CUUUCACCU 10  
Db 1:::|||||:  
31 CTTTCACCT 40

Search completed: March 19, 2003, 01:24:58  
Job time : 1321.5 secs

GenCore version 5.1.4-p5-4578  
copyright (c) 1993 - 2003 Compugen Ltd.

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Run on: March 18, 2003, 23:07:15 ; search time 991 seconds  
(without alignments)  
293.671 Million cell updates/sec

Title: US-09-702-498A-33  
Perfect score: 10  
Sequence: 1 CTCATCACCCCT 10

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: GEMBML;\*  
2: gb\_bp;\*  
3: gb\_hhg;\*  
4: gb\_in;\*  
4: gb\_on;\*  
5: gb\_ov;\*  
6: gb\_sts;\*  
7: gb\_dat;\*  
8: gb\_ph;\*  
9: gb\_pr;\*  
10: gb\_ro;\*  
11: gb\_sy;\*  
12: gb\_st;\*  
13: gb\_un;\*  
14: gb\_vl;\*  
15: em\_ba;\*  
16: em\_fun;\*  
17: em\_hum;\*  
18: em\_in;\*  
19: em\_mu;\*  
20: em\_on;\*  
21: em\_or;\*  
22: em\_ov;\*  
23: em\_dat;\*  
24: em\_ph;\*  
25: em\_pl;\*  
26: em\_ro;\*  
27: em\_sts;\*  
28: em\_vl;\*  
29: em\_vn;\*  
30: em\_btg\_hum;\*  
31: em\_btg\_inv;\*  
32: em\_btg\_other;\*  
33: em\_btg\_mus;\*  
34: em\_btg\_ph;\*  
35: em\_btg\_rcd;\*  
36: em\_btg\_men;\*  
37: em\_btg\_vrl;\*  
38: em\_sy;\*  
39: em\_btgo\_hum;\*  
40: em\_btgo\_mus;\*  
41: em\_btgo\_other;\*

## ALIGNMENTS

RESULT 1  
AX134713

LOCUS AX134713 DEFINITION Sequence 1 from Patent WO0132898. 10 bp DNA LINEAR  
ACCESSION AX134713 VERSION GI:14271230  
KEYWORDS SOURCE  
ORGANISM synthetic construct.  
artificial sequences.

REFERENCE 1 (bases 1 to 10)

AUTHORS Yonemitsu, Y., Hasagawa, M. and Alton, E.

TITLE Recombinant sendai virus vector for introducing exogenous genes to

Pred. No. is the number of results predicted by chance to have a

airway epithelia

Patent: WO 0132898-A 1 10-MAY-2001;

FEATURES Dnavec Research Inc. (JP) Location/Qualifiers  
 SOURCE 1. .10  
 /organism="synthetic construct"  
 /note="artificially synthesized sequence"  
 BASE COUNT 1 a 5 c 0 g 4 t  
 ORIGIN

RESULT 2  
 Query Match 100.0%; Score 10; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 QY 1 CTTTCACCT 10  
 |||||  
 Db 1 CTTTCACCT 10

FEATURES Dnavec Research Inc. (JP) Location/Qualifiers  
 SOURCE 1. .10  
 /organism="synthetic construct"  
 /note="artificially synthesized sequence"  
 BASE COUNT 1 a 5 c 0 g 4 t  
 ORIGIN

RESULT 3  
 Query Match 100.0%; Score 10; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 QY 1 CTTTCACCT 10  
 |||||  
 Db 1 CTTTCACCT 10

FEATURES Dnavec Research Inc. (JP) Location/Qualifiers  
 SOURCE 1. .10  
 /organism="synthetic construct"  
 /note="artificially synthesized sequence"  
 BASE COUNT 1 a 5 c 0 g 4 t  
 ORIGIN

RESULT 4  
 AR030044/c  
 LOCUS AR030044  
 DEFINITION Sequence 233 from patent US 5861244.  
 ACCESSION AR030044  
 VERSION AR030044.1 GI:5943258  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 12)  
 AUTHORS Wang, C.-G. and Hepburn, A.G.  
 TITLE Genetic sequence assay using DNA triple strand formation  
 JOURNAL Patent: US 5861244-A 233 19-JAN-1999;  
 Location/Qualifiers 1. .12

FEATURES Dnavec Research Inc. (JP) Location/Qualifiers  
 SOURCE 1. .10  
 /organism="synthetic construct"  
 /ab\_xref="txon:32630"  
 /note="Artificially synthesized Sequence"  
 BASE COUNT 5 a 0 c 6 g 1 t  
 ORIGIN

RESULT 5  
 AR099568  
 LOCUS AR099568  
 DEFINITION Sequence 95 from patent US 6077833.  
 ACCESSION AR099568  
 VERSION AR099568.1 GI:12809334  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Bennett, C. Frank. and Vickers, T.A.  
 TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
 JOURNAL Patent: US 6077833-A 95 20-JUN-2000;  
 Location/Qualifiers 1. .19

FEATURES Dnavec Research Inc. (JP) Location/Qualifiers  
 SOURCE 1. .10  
 /organism="unknown"  
 BASE COUNT 4 a 6 c 4 g 5 t  
 ORIGIN

RESULT 6  
 AR178849  
 LOCUS AR178849  
 DEFINITION Sequence 95 from patent US 6319906.  
 ACCESSION AR178849  
 VERSION AR178849.1 GI:20219987

Query Match 100.0%; Score 10; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 QY 1 CTTTCACCT 10  
 |||||  
 Db 7 CTTTCACCT 16

FEATURES Dnavec Research Inc. (JP) Location/Qualifiers  
 SOURCE 1. .10  
 /organism="unknown"  
 BASE COUNT 4 a 0 c 6 g 1 t  
 ORIGIN

Query Match 100.0%; Score 10; DB 6; Length 11;

KEYWORDS SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7-protein  
JOURNAL Patent: US 6319906-A 95-20-NOV-2001;  
FEATURES Source Location/Qualifiers  
1..19  
/organism="unknown"  
BASE COUNT 4 a 6 c 4 g 5 t  
ORIGIN

Query Match Best Local Similarity 100.0%; Score 10; DB 6; Length 19;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
Db 7 CTTCACCT 16

RESULT 7  
AX108449  
LOCUS AX108449  
DEFINITION Sequence 12 from Patent WO0123548.  
ACCESSION AX108449  
VERSION AX108449.1 GI:13923775  
KEYWORDS SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dorit,R.L. and Cole,K.B.  
TITLE DNA-cleaving nuclease p rna  
JOURNAL Patent: WO 0123548 A 12 05-APR-2001;  
FEATURES Source  
1..21  
'/organism="synthetic construct"  
'/db\_xref="taxon:32630"  
'/note="primer" 32630'  
BASE COUNT 7 a 10 g 3 t  
ORIGIN

Query Match Best Local Similarity 100.0%; Score 10; DB 6; Length 21;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
Db 21 CTTTCACCT 12

RESULT 8  
AX108450  
LOCUS AX108450  
DEFINITION Sequence 13 from Patent WO0123548.  
ACCESSION AX108450  
VERSION AX108450.1 GI:13923776  
KEYWORDS SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dorit,R.L. and Cole,K.B.  
TITLE DNA-cleaving nuclease p rna  
JOURNAL Patent: WO 0123548 A 13 05-APR-2001;  
FEATURES Source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
'/db\_xref="taxon:32630"  
'/note="Synthetic primer"

BASE COUNT 4 a 9 c 1 g 7 t  
ORIGIN

RESULT 9  
AX417439  
LOCUS AX417439  
DEFINITION Sequence 21 from Patent EP1197495.  
ACCESSION AX417439  
VERSION AX417439.1 GI:21522724  
KEYWORDS SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 Higashi,K. and Komatsu,K.  
AUTHORS Dna-binding protein Yb-1-containing collagen accumulation  
TITLE JOURNAL Patent: EP 1197495-A 21 17-APR-2002;  
FEATURES source  
1..21  
'/organism="synthetic construct"  
'/db\_xref="taxon:32630"  
'/note="Designed oligonucleotide primer to synthesize  
collagen alpha 1 probe" 32630'

BASE COUNT 6 a 4 c 8 g 3 t  
ORIGIN

Query Match Best Local Similarity 100.0%; Score 10; DB 6; Length 21;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
Db 11 CTTTCACCT 2

RESULT 10  
AX476918  
LOCUS AX476918  
DEFINITION Sequence 9 from Patent WO0220848.  
ACCESSION AX476918  
VERSION AX476918.1 GI:22216171  
KEYWORDS SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,  
Luisi,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.  
TITLE Gene and sequence variation associated with cancer  
JOURNAL Patent: WO 0220848-A 9 14-MAR-2002;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES Location/Qualifiers  
1..21  
'/organism="synthetic construct"  
'/db\_xref="taxon:32630"  
'/note="Synthetic primer"

BASE COUNT 4 a 9 c 1 g 7 t  
ORIGIN



Db 13 CTTTCACCT 4

	source	1..22	
RESULT	6 a /organism="Unknown"	5 g	
14	6 c	5 t	
BD010082	Query Match	100.0%; Score 10; DB 6; Length 22;	
ID BD010082	Best Local Similarity	100.0%; Pred. No. 1.8e+05; Mismatches 0;	
XX	Matches 10; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;	
AC BD010082;	Qy 1 CTTTCACCT 10	Db 10 CTTTCACCT 19	
XX			
SV BD010082.1	DT 08-FEB-2002 (Rel. 70, Created)	DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)	
XX	DE Paramyxovirus having modified transcription initiation sequence.	KW JP 03075813-T/12.	
XX	OS synthetic construct.	XX OC artificial sequence.	
XX	[1]	RN 1-21	
RP	RA Nagai Y., Kato A., Hasegawa M.;	RA Nagai Y., Kato A., Hasegawa M.;	
RL	RT "Paramyxovirus having modified transcription initiation sequence";	RT "Paramyxovirus having modified transcription initiation sequence";	
RL DNAMEC RESEARCH INC.YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.	RL DNAMEC RESEARCH INC.YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA.	XX	
CC OS Artificial Sequence	CC OS Artificial Sequence	CC OS Artificial Sequence	
CC PN JP 03075813-T/12	CC PN JP 03075813-T/12	CC PN JP 03075813-T/12	
CC PD 06-MAR-2001	CC PD 06-MAR-2001	CC PD 06-MAR-2001	
CC PP 06-SEP-1999 JP 99P 252231	CC PR 06-SEP-1999 JP 99P 252231	CC PR 06-SEP-1999 JP 99P 252231	
CC PT YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA	CC PT YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA	CC PT YOSHIIKU NAGAI,ATSUSHI KATO,MAMORU HASEGAWA	
CC PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00	CC PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00	CC PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00	
CC CC	CC CC	CC CC	
CC FH Key	CC FH Key	CC FH Key	
CC FT source	CC FT source	CC FT source	
CC FT	CC FT	CC FT	
XX FH	XX FH	XX FH	
KEY	Location/Qualifiers	KEY	
FT source	1..21	FT source	1..21
FT	/organism="Artificial Sequence"	FT	/organism="Artificial Sequence"
XX	Location/Qualifiers	XX	Location/Qualifiers
SQ	Sequence 21 BP; 7 A; 6 C; 4 G; 4 T; 0 other;	SQ	Sequence 21 BP; 7 A; 6 C; 4 G; 4 T; 0 other;
Qy	Query Match Best Local Similarity 100.0%; Score 10; DB 23; Length 21; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	Query Match Best Local Similarity 100.0%; Score 10; DB 23; Length 21; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 CTTTCACCT 10	Db	9 CTTTCACCT 18

RESULT 15

AR099567 LOCUS AR099567 DEFINITION Sequence 94 from patent US 6077833. linear PAT 14-FEB-2001

ACCESSION AR099567 VERSION AR099567.1 SOURCE Unknown ORGANISM Unknown

REFERENCE 1 (bases 1 to 22) AUTHORS Bennett,C.Frank, and Vickers,T.A. TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein Patent: US 6077833-A 94 20-JUN-2000; FEATURES Location/Qualifiers

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.4\_p5-4578  
 copyright (C) 1993 - 2003 Compugen Ltd.

Run on: March 18, 2003, 23:06:05 ; Search time 168 Seconds  
 (without alignments)  
 134.048 Million cell updates/sec

Title: US-09-702-498A-33  
 Perfect score: 10  
 Sequence: CTTTCACCTT 10

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

1: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/NA1980.DAT: \*  
 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT: \*  
 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT: \*  
 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT: \*  
 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT: \*  
 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT: \*  
 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT: \*  
 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT: \*  
 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT: \*  
 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT: \*  
 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT: \*  
 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT: \*  
 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT: \*  
 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT: \*  
 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT: \*  
 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT: \*  
 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT: \*  
 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT: \*  
 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT: \*  
 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT: \*  
 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT: \*  
 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT: \*  
 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT: \*  
 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT: \*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	10.00.0	10 22	AAT165896	Nucleotide sequence
2	10.00.0	10 22	AAT73613	DNA sequence; SEQ S sequence Oligonucleotide S
3	10.00.0	10 22	AAT23653	Sendai virus S seq
4	10.00.0	10 22	AAT86115	Modified transcript
5	10.00.0	10 22	AAT77598	Sendai virus S seq
6	10.00.0	10 24	AAL47265	Angiopeptins gene
7	10.00.0	10 24	AAL38107	DNA sequence #1 re
8	10.00.0	10 24	AAB48812	Sendai virus S Oli
9	10.00.0	10 24	ABL3904	
10	100.0	10		

**ALIGNMENTS**

RESULT ID	SEQUENCE	TYPE	DESCRIPTION
AAT15896	AAT15896 standard; DNA; 10 BP.	XX	
AC	AAT15896;	XX	
DT	03-JAN-2002 (first entry)	XX	
DE	Nucleotide sequence of a synthetic oligonucleotide.	XX	
KW	Vaccine; Sendai virus vector; viral protein; immunodeficiency virus; AIDS; antigen gene; nasal mucosa; lymph node; ss.	XX	
OS	Synthetic.	XX	
PN	WO200172340-A1.	XX	
PD	04-OCT-2001.	XX	
PF	30-MAR-2001; 2001WO-JP02769.	XX	
PR	30-MAR-2000; 2000US-193127P.	XX	
PA	(DNAV-) DNAV-E RES INC.	XX	
PA	(NINRA ) JAPAN NAT INST INFECTIOUS DISEASES.	XX	
PT	Kano M., Matano T., Kato A., Nagai Y., Hasegawa M.	XX	
DR	WPI: 2001-616443/71.	XX	
PT	Viral protein of immunodeficiency virus-encoding Sendai virus vector-based AIDS virus vaccine for provision of efficient protective	XX	

OM nucleic - nucleic search, using sw model

Human domain B2  
 Triple helix forming Oligonucleotide S  
 Oligonucleotide S  
 Oligonucleotide S  
 Oligonucleotide S  
 Modified transcript  
 Modified transcript  
 Modified transcript  
 Human DRD2 allele  
 Human DRD2 allele  
 Human DRD2 allele  
 Human DRD2 allele  
 Human CLCA1 gene  
 Human CLCA1 gene  
 Human CLCA1 gene  
 Human B7-2 target gene  
 Human B7-2 mRNA  
 PCR primer #1 from  
 Human familial ccc  
 Human FCH1 locus  
 Human B7-2 target  
 Human B7-2 mRNA  
 Angiotensinogen  
 Primer for detection  
 PCR primer used  
 Human angiotensin  
 Human angiotensin  
 Human DRD2 exon 6

PT immunity comprises nasal administration to e.g. macaque to suppress  
 XX onset and progress of AIDS -  
 PS Disclosure; Page 27; 92pp; Japanese.  
 PT  
 XX  
 CC The specification describes a vaccine containing a Sendai virus vector  
 CC which encodes the viral protein of immunodeficiency virus. The vaccine  
 CC is for treating AIDS, with expression of antigen gene mediated by the  
 CC vector in nasal mucosa and local lymph nodes detected and  
 CC antigen-specific cell-mediated response induced at significant  
 CC level after vaccination. The present sequence represents an  
 CC oligonucleotide which is used in the course of the invention.  
 XX SQ sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTCACCCCT 10  
 XX 1 ||||| 11111 10  
 Db 1 CTTTCACCCCT 10  
 RESULT 2  
 AAH73613  
 ID AAH73613 standard; DNA; 10 BP.  
 XX  
 AC AAH73613;  
 XX  
 DT 27-SEP-2001. (first entry)  
 DE DNA sequence, SEQ ID NO. 1.  
 XX  
 KW Gene therapy; vascular disorder; recombinant paramyxovirus vector; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200153491-A1.  
 XX  
 PR 19-JAN-2000; 2000JP-0014136.  
 PA (DNAV-) DNAYEC RES INC.  
 XX  
 PI Masaki I, Yonemitsu Y, Sueishi K, Hasegawa M, Kinoh H;  
 XX  
 DR 2001-457610/49.  
 PT paramyxovirus vector containing foreign gene for efficient gene  
 XX transfer into vascular cells -  
 PR disclosure; Page 19; 84pp; Japanese.  
 PS Disclosure; Page 19; 84pp; Japanese.  
 XX  
 CC The invention relates to a method for inserting nucleic acid into blood  
 CC vessel cells by contacting the cells with the nucleic acid contained in  
 recombinant paramyxovirus vector or cells transformed by it. The  
 CC method can be used for gene therapy of vascular disorders. Genes that  
 CC can be introduced into blood vessel cells by this method include cell  
 cycle regulators (such as p53, p21, p16 and p27), inhibitory factors  
 CC (such as H-Ras, eNOS and C-natriuretic peptide), ion channels (such as  
 CC Kir 6.2 potassium channel), blood proteins (such as urokinase and  
 CC tissue plasminogen activator), tissue factor pathway inhibitors (such  
 CC as TFP1) and vascular growth factors (such as vascular endothelial  
 CC growth factor (VEGF), fibroblast growth factor (FGF) and hepatocyte  
 CC growth factor (HGF)). The present sequence is provided in the  
 XX specification.  
 Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

XX  
 XX  
 KW Extracellular superoxide dismutase; EC-SOD; immunosuppressive;  
 KW antiinflammatory; antiarthritis; antirheumatic; arthritis; colitis;  
 KW systemic autoimmune disease; systemic lupus erythematosus;  
 KW rheumatic myocarditis; progressive systemic sclerosis; dermatomyositis;  
 KW Sjogren's syndrome; polyarteritis; Sendai virus; ss.  
 OS Parainfluenza virus.  
 XX  
 XX CA2316518-A1.  
 PN  
 XX  
 PD 01-MAR-2001.  
 XX  
 XX PF 31-AUG-2000; 2000CA-2316518.  
 XX  
 XX PR 01-SEP-1990; 99JP-0248032.  
 PR 27-APR-2000; 2000CA-2304453.  
 XX  
 PA (DNAV-) DNA VEC RES INC.  
 XX  
 PA (DNAV-) DNA VEC RES INC.  
 XX  
 PR 31-AUG-2000; 2000CA-2316518.  
 XX  
 PR 01-SEP-1990; 99JP-0248032.  
 PT Nagai Y, Kato A, Hasegawa M;  
 XX  
 DR WPI; 2001-244576/25.  
 XX  
 PT Paramyxovirus vectors with modified transcription initiation sequences  
 PT for increased expression of foreign genes in production of drugs and  
 PT vaccines.  
 XX  
 PS Disclosure: Page 24; 71PP; English.  
 XX  
 CC This invention relates to a superoxide dismutase (SOD) protein which  
 CC exists extracellularly and is termed EC-SOD, and the polynucleotide  
 CC encoding it. SOD is the enzyme that catalyses the reaction involved in  
 XX WPI; 2001-300717/32.  
 PT New EC-SOD Proteins and nucleic acids encoding the protein useful in  
 PT gene therapy for treating or preventing systemic autoimmune diseases,  
 e.g. rheumatoid arthritis, colitis and systemic lupus erythematosus.  
 XX  
 PS Disclosure: Page 24; 71PP; English.  
 XX  
 CC This invention relates to a superoxide dismutase (SOD) protein which  
 CC exists extracellularly and is termed EC-SOD, and the polynucleotide  
 CC encoding it. SOD is the enzyme that catalyses the reaction involved in  
 CC superoxide anion radical production. The invention includes a vector  
 CC containing the EC-SOD coding sequence, and a method for treating or  
 CC preventing systemic autoimmune diseases comprising administering the  
 CC vector. Methods using the EC-SOD protein and DNA sequences result in  
 CC immunosuppressive, anti-inflammatory, antiarthritic, and antirheumatic  
 CC activity. The EC-SOD protein and nucleic acid encoding the protein are  
 CC useful for treating systemic autoimmune diseases such as arthritis,  
 CC rheumatoid arthritis, colitis, systemic lupus erythematosus, rheumatic  
 CC myocarditis, progressive systemic sclerosis, dermatomyositis, polymyositis,  
 CC mixed connective tissue disease, Sjogren's syndrome, Polyarteritis, Wegener granulomatosis and colitis. The present  
 CC sequence represents a Sendai virus (Parainfluenza virus) oligonucleotide  
 CC which can be used in the construction of a vector containing the EC-SOD  
 CC gene.  
 XX  
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTCACCT 10  
 Db 1 CTTTCACCT 10  
 DE Sendai virus S sequence complement.  
 RESULT 6  
 ID AAL47265  
 ID AAL47265 standard; DNA; 10 BP.  
 XX  
 AC AAL47265;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Sendai virus S sequence complement.  
 XX  
 KW Sendai virus vector; gene therapy; antiinflammatory; inflammation;  
 KW cardiovascular system; paramyxovirus; IL-10; pulmonary fibrosis;  
 KW sclerosing peritonitis; prostatomegaly; multiple sclerosis;  
 KW neuroprotective; immunosuppressive; antidiabetic; antirheumatic;  
 KW transplant rejection; diabetes; chronic articular rheumatism;  
 KW psoriasis; inflammatory enteropathy; systemic lupus erythematosus;  
 KW iritis; granulomatous disease; chronic nephritis; scleroderma;  
 KW hysteroscopic; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.  
 OS Sendai virus.  
 XX  
 PN WO200238726-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 AC  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Modified transcription initiation site Paramyxovirus related oligo #18.  
 KW  
 XX Transcription initiation sequence; viral vector; vaccine; therapy; ds.  
 OS Unidentified.  
 XX  
 DR WPI; 2002-490069/52.

XX	XX	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
PT	PT	in which expression product of gene comprised in vector is transferred
PT	PT	to a site different from the site of administration through the
PT	PT	bloodstream -
XX	PS	Disclosure; Page 17; 67pp; English.
CC	CC	The present invention relates to a paramyxovirus vector for gene transfer
CC	CC	to the cardiovascular system, where the expression product of a gene
CC	CC	comprised in the vector is transferred to a site different from the site
CC	CC	of administration through the bloodstream. The vector is useful for
CC	CC	transferring sequences such as IL-10 to the cardiovascular system, for
CC	CC	treating pneumonia in cystic fibrosis patients and for treating
CC	CC	inflammatory diseases such as pulmonary fibrosis, sclerosing peritonitis,
CC	CC	prostacomegaly, multiple sclerosis, post transplant rejection, diabetes,
CC	CC	chronic articular rheumatism, psoriasis, inflammatory enteropathy,
CC	CC	systemic lupus erythematosus, iritis, granulomatous disease, chronic
CC	CC	nephritis, scleroderma, heterotonia, keloid and cirrhosis. The present
CC	CC	sequence is a DNA fragment used to produce the vector of the invention.
XX	SQ	Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
Query Match	Score 10;	DB 24;
Best Local Similarity	100.0%	Length 10;
Matches	10;	Conservative 0;
Indels	0;	Gaps 0;
Gaps	0;	
Query Match	Score 10;	DB 24;
Best Local Similarity	100.0%	Length 10;
Matches	10;	Conservative 0;
Indels	0;	Gaps 0;
Gaps	0;	
Qy	1	CRTTCACCT 10
Db	1	CRTTCACCT 10
RESULT 7	RESULT 8	
AAL38107	AABK48812	
ID	ID	AABK48812 standard; DNA; 10 BP.
XX	XX	
AAL38107;	AC	ABK48812;
XX	XX	
DT	DT	15-JUL-2002 (first entry)
15-AUG-2002 (first entry)	DE	DNA sequence #1 relating to paramyxovirus vector for gene transfer.
DE	XX	
Angiogenesis gene containing paramyxovirus vector related oligo #1.	KW	Method for gene transfer; skeletal muscle; paramyxovirus vector;
XX	KW	gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective;
KW	KW	myotrophic; insulin-like growth factor; IGF; ds.
OS	XX	
Unidentified.	OS	
PN	PN	WO200231138-A1.
XX	XX	
PD	PD	18-APR-2002.
XX	XX	
PF	PF	26-SEP-2001; 2001WO-JP08372.
XX	XX	
PR	PR	06-OCT-2000; 2000JP-0308533.
XX	XX	
PA	PA	(INAV-) DNAVEC RES INC.
XX	XX	
PI	PI	Hukumura M, Shiotani A, Maeda M, Hasegawa M;
XX	XX	
DR	DR	WPI; 2002-340180/37.
XX	XX	
PT	PT	Paramyxovirus vector for transferring foreign gene e.g. insulin-like
PT	PT	growth factor into skeletal muscle in gene therapy of neuromuscular
PT	PT	disorders.
OS	PS	
Unidentified.	Disclosure; Page 14; 56pp; Japanese.	
XX	CC	
XX	CC	The present invention relates to a method for transferring a foreign
XX	CC	gene into skeletal muscle. The method comprises administering a
XX	CC	paramyxovirus inserted with the foreign gene. The paramyxovirus vector
XX	CC	is useful for transferring a foreign gene e.g. insulin-like growth
PR	CC	factor (IGF) into skeletal muscle in the gene therapy of neuromuscular
27-NOV-2000; 2000JP-0359374.	CC	disorders. Such a vector can sustain transgene expression for up to a
XX	CC	month after injection and is safe, non-infective and does not cause
PA	CC	tumourigenesis. The present DNA sequence of unknown function is
(DNAV-) DNAVEC RES INC.	CC	given in the specification or the present invention.
XX	XX	
PT	Yonemitsu Y, Sueishi K, Fukumura M, Hou X, Hasegawa M;	
XX		
DR	WPI; 2002-452662/48.	
XX	Query Match	Score 10;
PT	Best Local Similarity	100.0%
PT	Matches	10;
PT	Indels	0;
PT	Gaps	0;
PS	Disclosure; Page 23; 94pp; Japanese.	
XX	Query Match	Score 10;
Query Match	Best Local Similarity	100.0%
Query Match	Matches	10;
Query Match	Indels	0;
Query Match	Gaps	0;
Qy	1	CRTTCACCT 10
Db	1	CRTTCACCT 10
RESULT 9	RESULT 9	
ABL3904	ABL3904	
ID	ID	ABL3904 standard; DNA; 10 BP.
XX	XX	
CC	The invention relates to a paramyxovirus vector containing an	
CC	angiogenesis gene, which can be used for gene therapy of ischaemia in	
CC	tissues including brain, heart, lung, skeletal muscle and kidney. The	
CC	expression of the virus vector is free from edema and specific tissues	
CC	can be targeted. This polynucleotide sequence represents an artificial	
CC	oligonucleotide relating to the paramyxovirus vector containing an	
CC	angiogenesis gene FGF2 of the invention.	

AC ABL39904;  
 XX  
 DT 14-MAY-2002 (first entry)  
 XX  
 DE Sendai virus S oligonucleotide SEQ ID NO:1.  
 XX  
 KW Sendai virus; virus vector; renal cell; paramyxovirus; gene transfer;  
 KW gene therapy; kidney; nephrotropic; antidiabetic; diabetes; renopathy;  
 KW chronic glomerulonephritis; glomerulosclerosis; Alport's syndrome;  
 KW tubulointerstitial nephritis; ss.  
 OS Parainfluenza virus.  
 XX  
 PN WO200200264-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PA 27-JUN-2001; 2001WO-JP05513.  
 XX  
 PR 27-JUN-2000; 2000JP-0197870.  
 XX  
 PA (DNAV-) DNAVEC RES INC.  
 XX  
 PI Imai E, Isaka Y, Fukumura M, Hasegawa M;  
 DR WPI; 2002-130841/17.  
 XX  
 PS Transferring a gene into renal cells, useful for gene therapy of a  
 PT kidney to treat e.g. chronic glomerulonephritis, comprises using a  
 PT virus vector, particularly of paramyxovirus  
 XX  
 PS Example 1, Page 38; 75pp; Japanese.  
 CC The present invention describes transferring a gene into renal cells  
 CC comprising contacting a paramyxovirus vector with the renal cells,  
 CC particularly by administration into blood vessels, especially the renal  
 CC artery or into the urethra. Also described are: (1) a paramyxovirus  
 CC vector for use in transferring a gene into renal cells; and  
 CC (2) compositions for transferring a gene into renal cells comprising  
 CC cells having the paramyxovirus vector or the vector. The method is used  
 CC for transferring a gene into renal cells. The virus is applicable in  
 CC gene therapy for the kidney to treat target diseases of e.g. chronic  
 CC glomerulonephritis, diabetes, nephropathy, glomerulosclerosis,  
 CC tubulointerstitial nephritis and Alport's syndrome. The transfer of a  
 CC gene into renal cells is with high efficiency, and after brief exposure,  
 CC the transferred gene is continuously expressed in renal cells over a  
 CC long period of time. The present sequence represents a Sendai virus  
 CC (parainfluenza virus) oligonucleotide which is used in an example from  
 XX  
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 Query Match 100.0%; Score 10; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4\_2e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTTTCACCC T 0  
 Db 11 CTTTCACCT 2  
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
 Query Match 100.0%; Score 10; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4\_3e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTTTCACCT 10  
 Db 11 CTTTCACCT 2  
 RESULT 11  
 AT118122;c  
 ID AT118122 standard; DNA; 11 BP.  
 XX  
 AC AT118122;  
 XX  
 DT 22-AUG-1996 (first entry)  
 DE Human dopamine D2 receptor DRD2 intron 6 polymorphic site (3208T).  
 XX  
 KW Dopamine D2 receptor; A1 allele; B1 allele; polymerase chain reaction;  
 KW PCR amplification of specific alleles; PASA; compulsive disorder;  
 KW cocaine dependence; alcoholism; genetic susceptibility; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key allele 6  
 FT Location/Qualifiers  
 FT /\*tag= a  
 FT /note= "nucleotides 3203-3213 of DRD2 in which  
 FT there is a T at the polymorphic position  
 XX  
 PN US5500343-A.  
 XX  
 AC AAQ57929/C  
 ID AAQ57929 standard; DNA; 11 BP.  
 XX  
 AC AAQ57929;  
 XX  
 DT 12-AUG-1994 (first entry)  
 XX  
 DE Oligonucleotide #1 to diagnose compulsive behaviour disorders.  
 XX  
 KW Human dopamine D2 receptor; genetic susceptibility; diagnosis;  
 KW DRD2; compulsive disorder; alcoholism; cocaine dependence;  
 XX

PD XX 19-MAR-1996.  
 XX PR 07-FEB-1990; 9005-0477057.  
 PF XX PI Hepburn AG, Wang C;  
 PT XX DR WPI; 1999-130384/11.  
 PR XX PT Assay of genetic sequences based on triplex formation from double  
 XX PT stranded analyte - and hybrid of anchor and reporter sequences, with  
 PA XX PT reporter released if triplex formation occurs, used e.g. to identify  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Blum K, Noble EP, Sheridan PJ;  
 XX DR WPI; 1996-171043/17.  
 XX PT Detecting genetic potential susceptibility to cocaine dependence or  
 PT alcoholism - by detecting human dopamine-D2 receptor gene A1 or B1  
 allele in the subject's DNA.  
 XX PR Example 3; Column 45; 56pp; English.  
 XX The dopamine D2 receptor DRD2(Ind-Ex7) haplotype is comprised of  
 CC two polymorphisms that are separated by 212 bp and span the  
 CC junction of the intron 6 and exon 7 sequences. The first is a T or  
 CC G at position 3208 and the second polymorphism is a T or C at  
 CC position 3420, providing 4 possible haplotypes. Haplotype I is  
 CC characterised by T at position 3208 and C at position 3420.  
 CC The primers #31208 and #3420 specifically amplify a 241 bp fragment  
 CC (3433-3193+1), beginning in intron 6 and ending in exon 7 of the  
 CC dopamine D2 receptor haplotype I which is associated with  
 CC genetic potential susceptibility to alcoholism in human subjects.  
 CC In particular, amplification is carried out using the PASA  
 CC technique (i.e. PCR Amplification of Specific Alleles). In related  
 CC methods, genetic potential susceptibility to cocaine dependence can  
 CC be detected by amplifying human dopamine D2 receptor A1 and B1  
 CC alleles (primers not specified).  
 XX SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
 XX Query Match 100.0%; Score 10; DB 17; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX ID AAX14846/C  
 XX ID AAX14846 standard; DNA; 12 BP.  
 XX AC AAX14846;  
 XX DT 24-MAR-1999 (first entry)  
 XX DE Triple helix forming nucleotides 384-395 of 23S rRNA gene.  
 XX KW Triple-helix forming region; Triplex formation; DNA detection;  
 KW Identification; bacteria; oncogene; virus; ds.  
 OS Leptospirura interrogans.  
 OS US5861244-A.  
 XX PD 19-JAN-1999.  
 XX DE 22-DEC-1993; 9305-0173489.  
 PF XX PR 24-JUN-1992; 9205-0826222.  
 PR XX PR 01-FEB-1990; 9005-0477057.  
 PR XX PR 23-JAN-1992; 9205-0826222.  
 PA XX PA (REGC ) UNIV CALIFORNIA.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Blum K, Noble EP, Sheridan PJ;  
 XX DR WPI; 1996-171043/17.  
 XX PT Detecting genetic potential susceptibility to cocaine dependence or  
 PT alcoholism - by detecting human dopamine-D2 receptor gene A1 or B1  
 allele in the subject's DNA.  
 XX PR Example 3; Column 45; 56pp; English.  
 XX The dopamine D2 receptor DRD2(Ind-Ex7) haplotype is comprised of  
 CC two polymorphisms that are separated by 212 bp and span the  
 CC junction of the intron 6 and exon 7 sequences. The first is a T or  
 CC G at position 3208 and the second polymorphism is a T or C at  
 CC position 3420, providing 4 possible haplotypes. Haplotype I is  
 CC characterised by T at position 3208 and C at position 3420.  
 CC The primers #31208 and #3420 specifically amplify a 241 bp fragment  
 CC (3433-3193+1), beginning in intron 6 and ending in exon 7 of the  
 CC dopamine D2 receptor haplotype I which is associated with  
 CC genetic potential susceptibility to alcoholism in human subjects.  
 CC In particular, amplification is carried out using the PASA  
 CC technique (i.e. PCR Amplification of Specific Alleles). In related  
 CC methods, genetic potential susceptibility to cocaine dependence can  
 CC be detected by amplifying human dopamine D2 receptor A1 and B1  
 CC alleles (primers not specified).  
 XX SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
 XX Query Match 100.0%; Score 10; DB 20; Length 12;  
 XX Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX ID AAX14846/C  
 XX ID AAX14846 standard; DNA; 12 BP.  
 XX AC AAX14846;  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 108723 for detecting SNP TSC0027206.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic;  
 KW Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX DE 06-APR-2001; 2001WO-1B00713.  
 XX KW 07-ABR-2000; 2000DE-1019173.  
 XX PR (EPIC- ) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX DE Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single nucleotide polymorphisms and cytosine  
 PT methylation status  
 XX PS Claim 1; SEQ ID 108723; 29pp + Sequence Listing; German.  
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

SQ

Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;

Query Match

100.0%

Score 10;

DB 23;

Length 13;

Best Local Similarity

100.0%

Pred. No. 4.3e+03;

Matches 10;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

QY

1 CTTTCACCT 10  
|||||||

Db

1 CTTTCACCT 10  
|||||||

SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;

Best Local Similarity 100.0%; Pred. No. 4.3e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
|||||||

Db 1 CTTTCACCT 10  
|||||||

RESULT

15 ABH2416/C

ID ABH2416 standard; DNA; 13 BP.

XX

AC ABH2416;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 224693 for detecting SNP TSC0054769.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001WO-1B00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX

PA (EPIC-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2001-657177/75.

XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

PS Claim 1; SEQ ID 224693; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and

CC AB10010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX

SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CTTTCACCT 10  
|||||||

Db

1 CTTTCACCT 10  
|||||||

wed Mar 19 09:04:46 2003

us-09-702-498a-33.rng

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

(without alignments)  
82.886 Million cell updates/sec

lure: 05-09-/02498A-33  
perfect score: 10  
Sequence: 1 CTTTCACCTT 10

Scoring table: IDENTITY\_NUC

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

**Post-processing:** Minimum Match 0%, Maximum Match 10%, Listing first 15%

Database : Issued\_Patents\_NA:\*

```
2: /cgn2_6/prtodata/1/ina/5B_COMBO.seq *
3: /cgn2_6/prtodata/1/ina/6A_COMBO.seq *
```

```

4 : /cgns2_6/Ptodata/1/ina/_6B__COMB.seq:*
5 : /cgns2_6/Ptodata/1/ina/_PCURS__COMB.seq:
6 : /cgns2_6/Ptodata/1/ina/_Pcurf1_les1

```

Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result Query & SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	10	100	9	1	1	
2	10	100	9	1	2	
3	10	100	9	1	3	
4	10	100	9	1	4	
5	10	100	9	1	5	
6	10	100	9	1	6	
7	10	100	9	1	7	
8	10	100	9	1	8	
9	10	100	9	1	9	
10	10	100	9	1	10	
11	10	100	9	1	11	
12	10	100	9	1	12	
13	10	100	9	1	13	
14	10	100	9	1	14	
15	10	100	9	1	15	
16	10	100	9	1	16	
17	10	100	9	1	17	
18	10	100	9	1	18	
19	10	100	9	1	19	
20	10	100	9	1	20	
21	10	100	9	1	21	
22	10	100	9	1	22	
23	10	100	9	1	23	
24	10	100	9	1	24	
25	10	100	9	1	25	
26	10	100	9	1	26	
27	10	100	9	1	27	
28	10	100	9	1	28	
29	10	100	9	1	29	
30	10	100	9	1	30	
31	10	100	9	1	31	
32	10	100	9	1	32	
33	10	100	9	1	33	
34	10	100	9	1	34	
35	10	100	9	1	35	
36	10	100	9	1	36	
37	10	100	9	1	37	
38	10	100	9	1	38	
39	10	100	9	1	39	
40	10	100	9	1	40	
41	10	100	9	1	41	
42	10	100	9	1	42	
43	10	100	9	1	43	
44	10	100	9	1	44	
45	10	100	9	1	45	
46	10	100	9	1	46	
47	10	100	9	1	47	
48	10	100	9	1	48	
49	10	100	9	1	49	
50	10	100	9	1	50	
51	10	100	9	1	51	
52	10	100	9	1	52	
53	10	100	9	1	53	
54	10	100	9	1	54	
55	10	100	9	1	55	
56	10	100	9	1	56	
57	10	100	9	1	57	
58	10	100	9	1	58	
59	10	100	9	1	59	
60	10	100	9	1	60	
61	10	100	9	1	61	
62	10	100	9	1	62	
63	10	100	9	1	63	
64	10	100	9	1	64	
65	10	100	9	1	65	
66	10	100	9	1	66	
67	10	100	9	1	67	
68	10	100	9	1	68	
69	10	100	9	1	69	
70	10	100	9	1	70	
71	10	100	9	1	71	
72	10	100	9	1	72	
73	10	100	9	1	73	
74	10	100	9	1	74	
75	10	100	9	1	75	
76	10	100	9	1	76	
77	10	100	9	1	77	
78	10	100	9	1	78	
79	10	100	9	1	79	
80	10	100	9	1	80	
81	10	100	9	1	81	
82	10	100	9	1	82	
83	10	100	9	1	83	
84	10	100	9	1	84	
85	10	100	9	1	85	
86	10	100	9	1	86	
87	10	100	9	1	87	
88	10	100	9	1	88	
89	10	100	9	1	89	
90	10	100	9	1	90	
91	10	100	9	1	91	
92	10	100	9	1	92	
93	10	100	9	1	93	
94	10	100	9	1	94	
95	10	100	9	1	95	
96	10	100	9	1	96	
97	10	100	9	1	97	
98	10	100	9	1	98	
99	10	100	9	1	99	
100	10	100	9	1	100	

C	C	1	10	100.0	11	1	US-0-909-383-1	Sequence 1, Applied Sequence
3	2	10	100.0	12	2	US-0-173-489C-233	Sequence 233, Applied Sequence	
3	10	100.0	19	3	US-08-777-266A-95	Sequence 95, Applied Sequence		

Sequence 95 / APP  
Sequence 94 / APP

7	10	100.0	23	4	US-07-952-422-7	Sequence 7, App
8	10	100.0	23	1	US-08-269-766-7	Sequence 7, App

9	10	100..0	23	1	US-08-319-55A-7	Sequence 7, Appl
10	10	100..0	23	2	US-08-319-55A-7	Sequence 7, Appl
11	10	100..0	23	3	US-08-319-55A-7	Sequence 7, Appl

				Sequence
				7, Appl
12	10	100.0	23	US-09-429-034-7
13	10	100.0	24	US-08-777-262A-93
14	10	100.0	24	US-09-351-100-02

C	15	100.0	124	4	US-08-325-632-39	Sequence 39, App
C	16	100.0	124	4	US-08-702-525-39	Sequence 39, App
C	17	100.0	124	4	US-08-702-525-39	Sequence 39, App

C C 17  
C 10 100.0 124 5 PCT-US95-03576-39  
C 18 100.0 333 3 US-09-009-913-15  
C 19 100.0 377 2 PCT-US-08-702-652-40

Patent No. 516805  
Sequence 2, Appl.

C	22	10	100.0	337	4	US-09-432-003-2	Sequence 2, App
C	23	10	100.0	438	4	US-09-432-006-56	Sequence 56, App
C	24	10	100.0	440	4	US-09-397-787-321	Sequence 321, App
C	25	10	100.0	584	4	US-09-328-111-83	Sequence 83, App
C	26	10	100.0	616	4	US-09-328-111-574	Sequence 574, App
C	27	10	100.0	650	4	US-09-328-111-189	Sequence 189, App

## ALIGNMENTS

Sequence 262, APP  
Sequence 72, APP  
Sequence 12, APP  
Sequence 12, APP  
Sequence 11, APP  
Sequence 11, APP  
Sequence 11, APP  
Sequence 28, APP  
Sequence 1462, AP  
Sequence 17, APP  
Sequence 2, APP11  
Patent No. 524298  
Sequence 9, APP1  
Sequence 57, APP1  
Sequence 128, APP  
Sequence 1, APP1  
Sequence 1, APP1

RESULT 1  
US-07-909-383-1c  
Sequence 1, Application US/07909383  
Patent No. 5500343

GENERAL INFORMATION:

APPLICANT: BLUM, KENNETH  
APPLICANT: NOBLE, E.P.  
APPLICANT: SHERIDAN, P.J.

TITLE OF INVENTION: ALLEGIC ASSOCIATION OF THE HUMAN  
TITLE OR INVENTION: DOPAMINE (D2) RECEPTOR GENE IN  
TITLE OF INVENTION: COMPULSIVE DISORDERS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/909, 383  
FILING DATE: 19920624  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HODGINS, DANIEL S.

REGISTRATION NUMBER: 31,026

REFERENCE/DOCKET NUMBER: UTSK:187

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-320-7200  
TELEX: 512-474-7577  
TELEX: NOT APPLICABLE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
REFERENCE: 31,026  
LENGTH: 11 base pairs  
TYPE: NUCLIC ACID  
STRANDINGNESS: single  
TOPOLOGY: linear

US-07-909-383-1

Query Match 100.0%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6e+02; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0;

ALIGNMENTS

Sequence 262, APP	Sequence 262, APP
Sequence 72, APP	Sequence 72, APP
Sequence 12, APP	Sequence 12, APP
Sequence 12, APP	Sequence 12, APP
Sequence 11, APP	Sequence 11, APP
Sequence 11, APP	Sequence 11, APP
Sequence 28, APP	Sequence 28, APP
Sequence 12, APP	Sequence 12, APP
Sequence 17, APP	Sequence 17, APP
Sequence 2, APP	Sequence 2, APP
Patent No. 5242798	Sequence 9, APP1
Sequence 9, APP1	Sequence 57, APP
Sequence 57, APP	Sequence 128, APP
Sequence 128, APP	Sequence 1, APP1
Sequence 1, APP1	Sequence 1, APP1

QY 1 CTTTCACCC 10

Db 11 CTTTCACCT 2

RESULT 2

US-08-173-489C-233/C

; Sequence 233, Application US/08173489C

; Patent No. 5861244

GENERAL INFORMATION:

APPLICANT: HEPBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA

TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: 510 EAST 73RD STREET,

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44MB storage

COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 5.2

SOFTWARE: WordPerfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 22 DEC 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATTORNEY/AGENT INFORMATION:

NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179

REFERENCE/DOCKET NUMBER: U9518-6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (attorney) (212) 708-1880

TELEFAX: (attorney) (212) 246-8959

INFORMATION FOR SEQ ID NO: 233:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs

TYPE: nucleic acid

STRANDEDNESS: double stranded

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

DESCRIPTION: 23S rRNA gene from Leptospira interrogans (Accession # X14249) nucleotides

DESCRIPTION: 384 to 395

HYPOTHETICAL: no

ANTI-SENSE: no

ORIGINAL SOURCE:

ORGANISM: Leptospira interrogans serovar canicola

STRAIN: moulton

PUBLICATION INFORMATION:

AUTHORS: Fukuba, M., Horie, I., Miuchi, T.

TITLE: Nucleotide sequence of a 23S

TITLE: ribosomal RNA gene for Leptospira interrogans

TITLE: serovar canicola strain moulton

JOURNAL: Nucleic Acids Research

VOLUME: 17

PAGES: 2123-2123

DATE: 1989

RELEVANT RESIDUES IN SEQ ID NO: 233 :FROM 1 TO 12

US-08-173-489C-233

Query Match 100.0% Score 10; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10

Db 7 CTTTCACCT 16

RESULT 3

US-08-77-266A-95

; Sequence 95, Application US/0877266A

; Patent No. 6077833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Expression of B7 Protein

TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Protein

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,266A

FILING DATE: December 31, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

US-08-77-266A-95

Query Match 100.0% Score 10; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10

Db 7 CTTTCACCT 16

RESULT 4

US-09-226-186B-95

; Sequence 95, Application US/09326186B

; Patent No. 6319906

GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank

TITLE: Oligonucleotide Compositions and Methods for the Expression of B7 Protein

TITLE: Modulation of the Expression of B7 Protein

FILE REFERENCE: ISPH-0376

CURRENT APPLICATION NUMBER: US/09/326,186B

CURRENT FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: 08/777,266

PRIOR FILING DATE: 1996-12-31

NUMBER OF SEQ ID NOS: 226

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 95

RESULT 5  
 US-08-777-266A-94  
 Sequence 94, Application US/08777266A  
 Patent No. 6077833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett

APPLICANT: Timothy A. Vickers

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins

TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-777-266A

FILING DATE: December 31, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPHE-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 22

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI SENSE: Yes

US-08-777-266A-94

Query Match 100.0%; Score 10; DB 3; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGACCC 10  
 Db 7 CTTCACCT 16

RESULT 5  
 US-08-777-266A-94  
 Sequence 94, Application US/08777266A  
 Patent No. 6077833

GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank

APPLICANT: Vickers, Timothy A.

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins

FILE REFERENCE: ISPH-0376

CURRENT APPLICATION NUMBER: US/09/326,186B

CURRENT FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: 08/777,266

PRIOR FILING DATE: 1996-12-31

NUMBER OF SEQ ID NOS: 226

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 94

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: Synthetic

US-09-326-186B-94

Query Match 100.0%; Score 10; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGACCC 10  
 Db 10 CTTCACCT 19

RESULT 7  
 US-07-952-442-7  
 Sequence 7, Application US/07952442  
 Patent No. 5374525

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaire, Xavier

APPLICANT: Linton, Richard P.

APPLICANT: Sourier, Florent

APPLICANT: Korelevsev, Youri

APPLICANT: Corval, Pierre

TITLE OF INVENTION: Angiotensinogen Gene Variants and Predisposition to Essential Hypertension

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue N.W., Suite 1000

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/952,442

FILING DATE: 19920930

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Innen, Jeffrey L.

REGISTRATION NUMBER: 28,957

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

RESULT 6  
 US-09-326-186B-94  
 Sequence 94, Application US/09326186B

Db      13 CTTTCACCC 22

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

RESULT 8  
US-08-269-766-7  
Sequence 7, Application US/08269766  
GENERAL INFORMATION:  
PATENT NO. 558584  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotalevtsiev, Youri  
APPLICANT: Corval, Pierre  
TITLE OF INVENTION: Angiotensinogen Gene Variants and Predisposition to Essential Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Verable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/269,766  
FILING DATE: 01-JUL-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19980-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-319-545A-7

Query Match      100.0%; Score 10; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
US-08-319-545A-7  
Sequence 7, Application US/08319545A  
GENERAL INFORMATION:  
PATENT NO. 5763168  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotalevtsiev, Youri  
APPLICANT: Corval, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition to Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Verable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-dos/MS-DOS  
SOFTWARE: WordPerfect 5.1/5.2 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,545A  
FILING DATE: 7-OCT-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19980-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-319-545A-7

Query Match      100.0%; Score 10; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
US-09-032-958-7  
Sequence 7, Application US/09032958B  
GENERAL INFORMATION:  
PATENT NO. 5993145  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent

Db      13 CTTTCACCC 22

Query Match      100.0%; Score 10; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTCACCC 10  
Db      13 CTTTCACCC 22

Db      13 CTTTCACCC 22

Query Match      100.0%; Score 10; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTCACCC 10  
Db      13 CTTTCACCC 22

APPLICANT: Kotolevtsiev, Youri  
 APPLICANT: Cottvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 TITLE OF INVENTION: to Hypertension  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1/5.2 Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/092,988  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/319,545  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 19780-104502-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-09-092-988-7

Query Match 100.0%; Score 10; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
 Db 13 CTTTCACCT 22

RESULT 11

PATENT NO. 6153386  
 GENERAL INFORMATION:  
 APPLICANT: Lalouel, Jean-Marc  
 APPLICANT: Jeunemaitre, Xavier  
 APPLICANT: Lofton, Richard P.  
 APPLICANT: Soubrier, Florent  
 APPLICANT: Kotolevtsiev, Youri  
 APPLICANT: Cottvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
 STREET: 555 Thirteenth Street N.W., Suite 701-E  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/106,216  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 09-/  
 FILING DATE: 08-JUN-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/319,545  
 FILING DATE: 07-OCT-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/952,545  
 FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 2323-124  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-783-6040  
 TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 23 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "primer"

US-09-106-216-7

Query Match 100.0%; Score 10; DB 3; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
 Db 13 CTTTCACCT 22

RESULT 12

US-09-429-034-7

; Sequence 7, Application US/09429034

; Patent No. 6165727

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc  
 APPLICANT: Jeunemaitre, Xavier  
 APPLICANT: Lofton, Richard P.  
 APPLICANT: Soubrier, Florent  
 APPLICANT: Kotolevtsiev, Youri  
 APPLICANT: Cottvol, Pierre  
 TITLE OF INVENTION: Method to Determine Predisposition  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1/5.2 Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/429,034  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/319,545  
FILING DATE: 7-OCT-1994  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502-2  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810  
TELEFAX: (609) 779-2400  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

US-09-429-034-7

RESULT 13

Query Match Best Local Similarity 100.0%; Score 10; DB 4; Length 23; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCTTCACCCCT 10
Db	13	CTTTCACCCCT 22

US-08-777-266A-93

Sequence 93, Application US/08777266A  
PATENT NO. 6077833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Proteins  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24

RESULT 14

Query Match Best Local Similarity 100.0%; Score 10; DB 3; Length 24; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCTTCACCCCT 10
Db	12	CTTTCACCCCT 21

US-09-326-186B-93

Sequence 93, Application US/09326186B  
PATENT NO. 6319906

GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.

TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Modulation of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO. 93  
LENGTH: 24

RESULT 15

Query Match Best Local Similarity 100.0%; Score 10; DB 4; Length 24; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCTTCACCCCT 10
Db	12	CTTTCACCCCT 21

US-08-205-697A-39/C

Sequence 39, Application US/08205697A  
PATENT NO. 6218510

GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.  
APPLICANT: Borriello, Francescopaolo  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LATIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US08/205,697A  
FILING DATE: 02-Mar-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandravouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: BWI-120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 107..124  
US-08-205-697A-39

Query Match 100.0%; Score 10; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY	1	CTTTCACCT	10
Db	13	CTTTCACCT	4

Search completed: March 19, 2003, 01:26:20  
Job time : 39 secs

**THIS PAGE BLANK (USPTO)**

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.4 p5\_4578

OM nucleic - nucleic search, using sw mode

Run on: March 19, 2003, 00:40:46 ; Search time 51.5 Seconds  
 (without alignments)  
 136.284 Million cell updates/sec

Title: US-09-702-498A-33

Perfect score: 10 CTTTACCCCT 10

Scoring table: IDENTITY\_NUC Gapov 10.0 , Gapext 1.0

Searched: 501302 seqs, 350932545 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published\_Applications\_NA.\*

1: /cgn2\_6/ptodata/1/pubpna/us07\_PUBCOMB.seq,\*  
 2: /cgn2\_6/ptodata/1/pubpna/PCV\_NEW\_PUB.seq,\*  
 3: /cgn2\_6/ptodata/1/pubpna/us06\_NEW\_PUB.seq,\*  
 4: /cgn2\_6/ptodata/1/pubpna/us06\_PUBCOMB.seq,\*  
 5: /cgn2\_6/ptodata/1/pubpna/us07\_NEW\_PUB.seq,\*  
 6: /cgn2\_6/ptodata/1/pubpna/PCVUS\_PUBCOMB.seq,\*  
 7: /cgn2\_6/ptodata/1/pubpna/us08\_NEW\_PUB.seq,\*  
 8: /cgn2\_6/ptodata/1/pubpna/us08\_PUBCOMB.seq,\*  
 9: /cgn2\_6/ptodata/1/pubpna/us09\_NEW\_PUB.seq,\*  
 10: /cgn2\_6/ptodata/1/pubpna/us10\_NEW\_PUB.seq,\*  
 11: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq,\*  
 12: /cgn2\_6/ptodata/1/pubpna/us60\_NEW\_PUB.seq,\*  
 13: /cgn2\_6/ptodata/1/pubpna/us60\_PUBCOMB.seq,\*  
 14: /cgn2\_6/ptodata/1/pubpna/us60\_PUBCOMB.seq,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

\* SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	100.0	10	9 US-09-966-277-63 Sequence 63, Appl
2	10	100.0	10	9 US-09-966-930-63 Sequence 63, Appl
3	10	100.0	10	9 US-09-966-930-63 Sequence 1, Appl
4	10	100.0	21	10 US-09-912-331-21 Sequence 21, Appl
5	10	100.0	30	9 US-09-988-115A-43 Sequence 43, Appl
6	10	100.0	47	9 US-09-966-277-43 Sequence 43, Appl
7	10	100.0	47	9 US-09-966-277-44 Sequence 43, Appl
8	10	100.0	47	9 US-09-966-930-43 Sequence 43, Appl
9	10	100.0	47	9 US-09-966-930-44 Sequence 44, Appl
10	10	100.0	63	10 US-09-823-699-10 Sequence 10, Appl
11	10	100.0	69	10 US-09-471-840-2 Sequence 2, Appl
12	10	100.0	69	10 US-09-471-840-2 Sequence 4, Appl
13	10	100.0	69	10 US-09-728-207-2 Sequence 2, Appl
14	10	100.0	69	10 US-09-728-207-2 Sequence 4, Appl
15	10	100.0	69	10 US-09-728-207-2 Sequence 2, Appl
16	10	100.0	72	9 US-09-966-277-34 Sequence 34, Appl
17	10	100.0	72	9 US-09-966-277-51 Sequence 51, Appl
18	10	100.0	72	9 US-09-966-277-52 Sequence 52, Appl
19	10	100.0	72	9 US-09-966-930-34 Sequence 34, Appl

ALIGNMENTS

RESULT 1  
 US-09-966-277-63

# Sequence 63, Application US/09966277  
 ; Patent No. US20020109306A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIRIZATO, Kaito  
 ; APPLICANT: SHIO, Tatsugumi  
 ; APPLICANT: KUNI, Hidekazu  
 ; APPLICANT: UEDA, Yasuji  
 ; APPLICANT: ASAKAWA, Makoto  
 ; APPLICANT: HASEGAWA, Manorou  
 ; APPLICANT: ITIDA, Akihito  
 ; APPLICANT: TOKITOU, Fumio  
 ; APPLICANT: TOKUSUMI, Takehiro  
 ; APPLICANT: INOUE, Makoto  
 ; APPLICANT: ITO, Toshiaki  
 ; APPLICANT: HIRATA, Fumio  
 ; APPLICANT: TOKUSUMI, Takeyoshi

TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS  
 FILE REFERENCE: 50026/028001  
 CURRENT APPLICATION NUMBER: US/09/966,277  
 CURRENT FILING DATE: 2001-03-27  
 PRIOR APPLICATION NUMBER: PCT/JP00/03195  
 PRIOR FILING DATE: 2000-05-18  
 PRIOR APPLICATION NUMBER: JP 2000/281451  
 PRIOR FILING DATE: 2001-09-18  
 PRIOR APPLICATION NUMBER: JP 11/200739  
 PRIOR FILING DATE: 1999-05-18  
 NUMBER OF SEQ ID NOS: 64  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 63  
 LENGTH: 10  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Artificially Synthesized Sequence  
 US-09-966-277-63

Query Match Score 100.0%; Score 10; DB 9; Length 10;  
 Best local Similarity 100.0%; Pred. No. 1 5e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACCCCT 10

Db 1 CTTTCACCT 10  
 RESULT 2 965-930-63  
 ; Sequence 63, Application US-09966930  
 ; Publication No. US20030022376A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KITAATO, Kai  
 ; APPLICANT: KUMA, Hidekazu  
 ; APPLICANT: OEDA, Yasuji  
 ; APPLICANT: ASAKAWA, Makoto  
 ; APPLICANT: HASOGAWA, Mamoru  
 ; APPLICANT: IIDA, Akihiro  
 ; APPLICANT: HIRATA, Takahiro  
 ; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
 ; FILE REFERENCE: 50026/029001  
 ; CURRENT APPLICATION NUMBER: US-09/965,930  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/03194  
 ; PRIOR FILING DATE: 2000-05-18  
 ; PRIOR APPLICATION NUMBER: JP 2001/203451  
 ; PRIOR FILING DATE: 2001-05-18  
 ; PRIOR APPLICATION NUMBER: JP 11/200740  
 ; PRIOR FILING DATE: 1999-05-18  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 63  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Artificially Synthesized Sequence  
 ; US-09-965-930-63

Query Match 100.0%; Score 10; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 10; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10  
 Db 1 CTTTCACCT 10

---

RESULT 3  
 US-09-822-699-1  
 ; Sequence 1, Application US-09823699  
 ; Patent No. US2002002143A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kano, Munehide  
 ; APPLICANT: Matano, Tetsuro  
 ; APPLICANT: Kato, Atsushi  
 ; APPLICANT: Nagai, Yoshiyuki  
 ; APPLICANT: Hasogawa, Mamoru  
 ; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus  
 ; FILE REFERENCE: 50026/022002  
 ; CURRENT APPLICATION NUMBER: US-09/823,699  
 ; CURRENT FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/193,127  
 ; PRIOR FILING DATE: 2000-03-30  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: artificially synthesized sequence  
 ; US-09-822-699-1

Query Match 100.0%; Score 10; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 10; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10  
 Db 1 CTTTCACCT 10

---

RESULT 4  
 US-09-972-331-21/c  
 ; Sequence 21, Application US-09972331  
 ; Patent No. US20030091083A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HIGASHI, KIYOSHI  
 ; APPLICANT: KOMATSU, KIYOSHI  
 ; TITLE OF INVENTION: DNA-BINDING PROTEIN YB-1-CONTAINING  
 ; FILE REFERENCE: 7372/72170  
 ; CURRENT APPLICATION NUMBER: US-09/972,331  
 ; CURRENT FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: JP 2000/310624  
 ; PRIOR FILING DATE: 2000-10-11  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 21  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: DESIGNED OLIGONUCLEOTIDE PRIMER TO SYNTHESIZE  
 ; OTHER INFORMATION: COLLAGEN ALPHA 1 PROBE  
 ; US-09-972-331-21

Query Match 100.0%; Score 10; DB 10; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 10; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 CTTTCACCT 10  
 Db 11 CTTTCACCT 2

---

RESULT 5  
 US-09-988-115A-43  
 ; Sequence 43, Application US-09988115A  
 ; Publication No. US2003003747A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robl, James M.  
 ; APPLICANT: Goldsby, Richard A.  
 ; APPLICANT: Ferguson, Stacy E.  
 ; APPLICANT: Kuroiwa, Yoshina  
 ; APPLICANT: Tomizuka, Kazuma  
 ; APPLICANT: Ishida, Isao  
 ; TITLE OF INVENTION: Expression of Xenogenous (Human)  
 ; TITLE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates  
 ; FILE REFERENCE: 50195/00803  
 ; CURRENT APPLICATION NUMBER: US/09/988,115A  
 ; CURRENT FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/311,625  
 ; PRIOR FILING DATE: 2001-08-09  
 ; PRIOR APPLICATION NUMBER: US 60/256,458  
 ; PRIOR FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: US 09/714,185  
 ; PRIOR FILING DATE: 2000-11-17  
 ; PRIOR APPLICATION NUMBER: US 60/156,410  
 ; PRIOR FILING DATE: 1999-11-19  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 43  
 ; LENGTH: 30  
 ; TYPE: DNA

ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Primer  
; US-09-988-115A-43

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	10;	100.0%	10;	9;	30;	0;	0;
Oy	1	CTTTCACCCCT	10				
Db	11	CTTTCACCCCT	20				

RESULT 6  
US-09-966-277-43/C  
; Sequence 43, Application US/09966277  
; Patent No. US20020169306A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, KaiO  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: KUMA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: TOKITOU, Fumino  
; APPLICANT: HIRATA, Takahiro  
; APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: VECTOR  
; FILE REFERENCE: 50026/028001  
; CURRENT APPLICATION NUMBER: US/09/966, 277  
; CURRENT FILING DATE: 2001-09-27  
; PRIORITY APPLICATION NUMBER: PCT/JP00/03195  
; PRIORITY FILING DATE: 2000-05-18  
; PRIORITY APPLICATION NUMBER: JP 2001/283451  
; PRIORITY FILING DATE: 2001-09-18  
; PRIORITY APPLICATION NUMBER: JP 11/200739  
; PRIORITY FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
; US-09-966-277-43

RESULT 8  
US-09-966-930-43/C  
; Sequence 43, Application US/09966930  
; Publication No. US20030022376A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, KaiO  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: KUMA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: HIRATA, Takahiro  
; APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
; FILE REFERENCE: 50026/029001  
; CURRENT APPLICATION NUMBER: US/09/966, 930  
; CURRENT FILING DATE: 2001-09-27  
; PRIORITY APPLICATION NUMBER: PCT/JP00/03194  
; PRIORITY FILING DATE: 2000-05-18  
; PRIORITY APPLICATION NUMBER: JP 2001/283451  
; PRIORITY FILING DATE: 2001-09-18  
; PRIORITY APPLICATION NUMBER: JP 11/200740  
; PRIORITY FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
; US-09-966-930-43

RESULT 7  
US-09-966-277-44  
; Sequence 44, Application US/09966277  
; Patent No. US20020169306A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, KaiO  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: RUMA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: TOKITOU, Fumino

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	10;	100.0%	Pred. No. 1.8e+03;	9;	47;	0;	0;
Oy	1	CTTTCACCCCT	10				
Db	13	CTTTCACCCCT	4				

RESULT 7  
US-09-966-277-44  
; Sequence 44, Application US/09966277  
; Patent No. US20020169306A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, KaiO  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: RUMA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: TOKITOU, Fumino

	Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	10;	100.0%	Pred. No. 1.8e+03;	9;	47;	0;	0;
Oy	1	CTTTCACCCCT	10				
Db	13	CTTTCACCCCT	4				

Db 13 CTTTCACCT 4

RESULT 9

US-09-866-930-44

Sequence 44, Application US/09966930

Publication No. US20030022376A1

GENERAL INFORMATION:

APPLICANT: KITAZATO, Kaito

APPLICANT: SHU, Tsugumine

APPLICANT: KIMA, Hidekazu

APPLICANT: UEDA, Yasuji

APPLICANT: ASAKAWA, Makoto

APPLICANT: HASEGAWA, Mamoru

APPLICANT: ITADA, Akihiro

APPLICANT: HIRATA, Takahiro

APPLICANT: INOUE, Makoto

TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP

FILE REFERENCE: 50026/029001

CURRENT APPLICATION NUMBER: US/09/966,930

CURRENT FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: PCT/JP00/03194

PRIOR FILING DATE: 2000-05-18

PRIOR APPLICATION NUMBER: JP 2001/283451

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: JP 11/200740

PRIOR FILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 44

LENGTH: 47

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-930-44

Query Match 100.0%; Score 10; DB 9; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CTTTCACCT 26

RESULT 10

US-09-823-639-10

Sequence 10, Application US/09823699

Patent No. US2002002143A1

GENERAL INFORMATION:

APPLICANT: Kano, Munehide

APPLICANT: Matano, Tetsuro

APPLICANT: Kato, Atsushi

APPLICANT: Nagai, Yoshiyuki

APPLICANT: Hasegawa, Mamoru

TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus

TITLE OF INVENTION: Vector

FILE REFERENCE: 50026/022002

CURRENT APPLICATION NUMBER: US/09/823,699

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 60/193,127

PRIOR FILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 63

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: artificially synthesized sequence

US-09-823-639-10

Query Match 100.0%; Score 10; DB 10; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CTTTCACCT 26

RESULT 11

US-09-471-840-2

Sequence 2, Application US/09471840

Patent No. US20020031706A1

GENERAL INFORMATION:

APPLICANT: NAGAI, Yoshiyuki

APPLICANT: KATO, Atsushi

APPLICANT: MURAI, Fukashi

APPLICANT: ASAKAWA, Makoto

APPLICANT: SAKATA, Tsuneki

APPLICANT: HASEGAWA, Mamoru

APPLICANT: SHIODA, Tatsuo

TITLE OF INVENTION: Negative Strand RNA Viral Vector Having Autonomous Replication Capability

FILE REFERENCE: 50026/004002

CURRENT APPLICATION NUMBER: US/09/471,840

CURRENT FILING DATE: 1999-12-23

EARLIER APPLICATION NUMBER: JP HEI 7-308315

EARLIER FILING DATE: 1995-10-31

EARLIER APPLICATION NUMBER: PCT/JP96/03068

EARLIER FILING DATE: 1996-10-22

EARLIER APPLICATION NUMBER: 09/070,938

EARLIER FILING DATE: 1998-04-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 69

TYPE: DNA

ORGANISM: Human Immunodeficiency Virus

FEATURE:

NAME/KEY: variation

LOCATION: (35)..(35)

OTHER INFORMATION: v at 35 is a, c, or g, not t or u.

US-09-471-840-2

Query Match 100.0%; Score 10; DB 10; Length 69;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 CTTTCACCT 26

RESULT 12

US-09-471-840-4

Sequence 4, Application US/09471840

Patent No. US20020031706A1

GENERAL INFORMATION:

APPLICANT: NAGAI, Yoshiyuki

APPLICANT: KATO, Atsushi

APPLICANT: MURAI, Fukashi

APPLICANT: ASAKAWA, Makoto

APPLICANT: SAKATA, Tsuneki

APPLICANT: HASEGAWA, Mamoru

APPLICANT: SHIODA, Tatsuo

TITLE OF INVENTION: Negative Strand RNA Viral Vector Having Autonomous Replication Capability

FILE REFERENCE: 50026/004002

CURRENT APPLICATION NUMBER: US/09/471,840

CURRENT FILING DATE: 1999-12-23

EARLIER APPLICATION NUMBER: JP HEI 7-308315

EARLIER FILING DATE: 1995-10-31

EARLIER APPLICATION NUMBER: PCT/JP96/03068

; EARLIER FILING DATE: 1996-10-22  
; EARLIER APPLICATION NUMBER: 09/070,938  
; EARLIER FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 69  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Chemical synthesis  
; US-09-471-840-4

Query Match 100.0%; Score 10; DB 10; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 16 CTTTCACCT 25

RESULT 13

US 09-728-207-2

; Sequence 2, Application US/09728207

; Patent No. US20020098576A1

GENERAL INFORMATION:

; APPLICANT: NAGAI, Yoshiyuki

; APPLICANT: KATO, Atsushi

; APPLICANT: MORAI, Fukashi

; APPLICANT: SAKATA, Tsuneaki

; APPLICANT: HASEGAWA, Mamoru

; APPLICANT: SHIODA, Tatsuo

TITLE OF INVENTION: Recombinant Sendai Virus

FILE REFERENCE: 50026/005001

CURRENT APPLICATION NUMBER: US/09-728,207

PRIORITY APPLICATION NUMBER: US/09/071,591

PRIORITY FILING DATE: 1998-05-01

PRIORITY APPLICATION NUMBER: JP HEI 7-285417

PRIORITY FILING DATE: 1995-11-01

PRIORITY APPLICATION NUMBER: PCT/JP96/03069

PRIORITY FILING DATE: 1996-10-22

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 69

TYPE: DNA

ORGANISM: Human immunodeficiency virus

FEATURE: variation

LOCATION: (35)..(35)

; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.

US-09-728-207-2

Query Match 100.0%; Score 10; DB 10; Length 69;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTTTCACCT 10

Db 17 CTTTCACCT 26

RESULT 14

US-09-728-207-4

; Sequence 4, Application US/09728207

; Patent No. US20020098576A1

GENERAL INFORMATION:

; APPLICANT: NAGAI, Yoshiyuki

; APPLICANT: KATO, Atsushi

; APPLICANT: MORAI, Fukashi

; APPLICANT: SAKATA, Tsuneaki

APPLICANT: HASEGAWA, Mamoru  
APPLICANT: SHIODA, Tatsuo  
TITLE OF INVENTION: Recombinant Sendai Virus  
FILE REFERENCE: 50026/005001  
CURRENT APPLICATION NUMBER: US/09-728,207  
CURRENT FILING DATE: 2000-12-01  
PRIORITY APPLICATION NUMBER: US/09/071,591  
PRIORITY FILING DATE: 1998-05-01  
PRIORITY APPLICATION NUMBER: JP HEI 7-285417  
PRIORITY FILING DATE: 1995-11-01  
PRIORITY APPLICATION NUMBER: PCT/JP96/03069  
PRIORITY FILING DATE: 1996-10-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSEQ for Windows Version 3.0  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Chemical synthesis  
; US-09-728-207-4

RESULT 15

US 09-070-938-2

; Sequence 2, Application US/09070938

; Patent No. US2002010066A1

GENERAL INFORMATION:

; APPLICANT: Nagai, Yoshiyuki

; APPLICANT: Kato, Atsushi

; APPLICANT: Morai, Fukashi

; APPLICANT: Asakawa, Makoto

; APPLICANT: Sakata, Tsuneaki

; APPLICANT: Hasegawa, Mamoru

; APPLICANT: Shioda, Tatsuo

TITLE OF INVENTION: Negative Strand RNA Viral

TITLE OF INVENTION: Vector Having Autonomous Replication Capability

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark &amp; Elbing LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,938

FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-308315

FILING DATE: 31-OCT-1995

APPLICATION NUMBER: JPP95/03068

FILING DATE: 22-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T

REGISTRATION NUMBER: 30,152

REFERENCE/DOCKET NUMBER: 50026/004001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
US-09-070-938-2

Query Match 100.0%; Score 10; DB 10; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 10; Conservative 0; Mismatches 0;  
Matches 10; Conservative 0; Mismatches 0;

QY 1 CTTCACCC 10  
||| |||||  
Db 17 CTTCACCT 26

Search completed: March 19, 2003, 02:47:57  
Job time : 51.5 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: March 18, 2003, 23:53:50 ; Search time 1320.5 Seconds

Perfect score: 10  
Sequence: 1 CTTTCACCC 10

**Scoring table: IDENTITY\_NUC**

Searched: 16154066 seqs, 8097743376 residues

[ 1 ]

卷之三

National Match 10  
Listing first 45

卷之三

ESTIN: \*

```
6: em_estpl:*
```

9: gb\_est1:\*

12: gb\_est3: \*

15: em estfun::  
16:    yvec::

卷之三

20: em\_gss\_p1h  
31: em\_gss\_virt

23: em\_gss\_mam  
24: --

26: em\_gss\_pro;

**pred.**: No. is the number of results predicted by chance to have a

... *and following my analysis of the total score distribution.*

No.	Score	Match	Length	DB	IP	Description
-----	-------	-------	--------	----	----	-------------

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
------------	-------	--------------------	-------	-------------

**RESULT** 1  
**TA285H020**  
**LOCUS** TA285H020  
**DEFINITION** T. brucei sheared genomic DNA clone 285h02, reverse sequence,  
**ACCESSION** AL485473  
**VERSION** AL485473.1  
**KEYWORDS** GSS.  
**SOURCE** Trypanosoma brucei.  
**ORGANISM** *Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;*  
**REFERENCE** 1-  
*Trypanosoma; Trypanosomatidae;*

ALIGNMENTS

Barrell, Oxford University Press, 1999'.  
 Email: [mlsayed@tgtr.org](mailto:mlsayed@tgtr.org)  
 Details of *T. brucei* sequencing at the Sanger Centre are available  
 at <http://www.sanger.ac.uk/projects/T-brucei/>.  
**FEATURES**

**source**

1. 28

/organism="Trypanosoma brucei"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="485h02"

Db

9 CTTTCACCT 18

**BASE COUNT**  
**ORIGIN**

Query Match

Best

Local

Similarity

100.0%

Score

10

DB

17

Length

28

;

Pred.

No.

7.8e+04

;

Matches

10

;

Conservative

0

;

Mismatches

0

;

Indels

0

;

Gaps

0

;

Oy

1

CTTTCACCT

10

;

Db

19

CTTTCACCT

10

;

BASE COUNT

ORIGIN

**BASE COUNT**  
**ORIGIN**

Query Match

Best

Local

Similarity

100.0%

Score

10

DB

17

Length

28

;

Pred.

No.

8.3e+04

;

Matches

10

;

Conservative

0

;

Mismatches

0

;

Indels

0

;

Gaps

0

;

Oy

1

CTTTCACCT

10

;

Db

19

CTTTCACCT

10

;

**RESULT 2****LOCUS**

AZ332275/c

**DEFINITION**

1M0060MLR

Mouse

10kb

Plasmid

UGCG1M

library

Mus

musculus

genomic

clone

UNGC1M0060MLR

R,

DNA

sequence.

**REFERENCE**

A2332275

**VERSION**

A2332275.1

**GSS****KEYWORDS****SOURCE****ORGANISM****Mus musculus****COMMENT****JOURNAL****REFERENCE****AUTHORS**

processed for submission. T-DNA derived sequences were "removed"

BASE COUNT ORIGIN	8 a	10 c	8 g	17 t
----------------------	-----	------	-----	------

```

Query Match          100.0%; Score 10; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches 10; Conservative 0; Mismatches 0;
Qy      1 CTCAGCACCT 10
       ||||| | |
Db      33 CTTCACCC 42

```

BASE COUNT	23 a	13 c	17 g	14 t	and selected for ampicillin resistance."
ORIGIN					
Query Match	100.0%	Score 10;	DB 17;	Length 67;	
best Local Similarity	100.0%	Pred. No. 9.4e+04;			
Matches 10; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0	
Qy 1 CTTTCACCC 10					
Db 34 CTTTCACCC 25					

**RESULT 4**  
**A2805524/c**  
**KEYWORD**  
**LOCUS** A2805524 67 bp DNA linear GSS 20-FEB-2001  
**DEFINITION** 2M0066P22R Mouse 10kb plasmid UGGC1M library Mus musculus genomic  
**ACCESSION** clone JUGC2M0066P22 R, DNA sequence.  
**VERSION** A2805524.1  
**GSS** A2805524.1 GI:12966335

SOURCE	house mouse.
ORGANISM	<i>Mus musculus</i>
REFERENCE	Bukarrotta; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases 1 to 10kb)
AUTHORS	Dunn,D., Avogay,A., Barber,M., Beacon,T., Duval,B., Hamil,C., Islam,H., Longaire,S., Mahmoud,M., Meenah,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: daunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0066 row: P column: 22  
Seq Primer: CACAGGGAAACGCGATGACC  
Class: plasmid ends  
High quality sequence stop: 67.

**FEATURES**  
 source  
 location/Qualifiers  
 1. .-57  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2K0066522"  
 /clone.lib="Mouse 10kb plasmid uuscm library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="vector: PWD2nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male); was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.Jax.org/resources/documents/dnare/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adapter oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptored DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD2 (9114732114 [gb] AF121972.1), a copy number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptored mouse DNA was annealed to  
 adaptored vector DNA, and transformed into

	BASE COUNT	23	a	13	c	17	g	.14	t
RESULT	5	Query Match Best Local Similarity Matches 10; conservative 0; Mismatches 0; Indels 0; Gaps 0							
ORIGIN		Best Local Similarity 100.0%; Pred. No. 9.4e+04; Mismatches 0; Indels 0; Gaps 0							
QY	1	CTTCACCC	T	10					
Db	34	CTTCACCC	T	25					
FEATURES	Source	Organism: Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo. Tissue: Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. CDNA Library Preparation: David B. Krizman, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center found through the T.M.A.G.E Consortium/LNBL, send email to: info@tmgainfo.llnl.gov Possible reversed clone: PolyA not found Seq primer: -400P from Gibco.							
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov 1 (bases 1 to 68) R_Emmert-Buck, M.D., Ph.D. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), JOURNAL: Unpublished (1997)							
REFERENCE	AUTHORS	Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. CDNA Library Preparation: David B. Krizman, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center found through the T.M.A.G.E Consortium/LNBL, send email to: info@tmgainfo.llnl.gov Possible reversed clone: PolyA not found Seq primer: -400P from Gibco.							
BASE COUNT	ORIGIN	26	a	8	c	22	g	12	t
RESULT	6	Query Match Best Local Similarity 100.0%; Score 10; DB 10; Length 68; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
LOCUS	DB	1	CCTTCACCC	T	10				
QY	57	CCTTCACCC	T	48					

DEFINITION kh35e05.y1 Ascaris suum male head pamp1 v2 Chiapelli McCarter  
 ACCESSION AZ781553  
 VERSION Az781553.1 GI:12914361  
 VERSION BT783611  
 KEYWORD EST  
 SOURCE pig roundworm.  
 ORGANISM Ascaris suum  
 Ascarioata; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea  
 Ascarididae; Ascaris.  
 REFERENCE 1 (bases 1 to 72)  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,  
 Dante,M., Marra,M., Hiller,L., Kuwabara,T., Theising,B., Bowers,Y.,  
 Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarakishevill,R.,  
 Ronko,I., Kennedy,S., Macquire,L., Beck,C., Underwood,K., Sheptoe,  
 M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,  
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and  
 Wilson,R.  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wuston.wustl.edu  
 The library was constructed by Brandi Chiapelli and Dr. James  
 McCarter at Washington University, St. Louis. The cDNA was made by  
 using Dynabead Oligo-dT priming (Dynal). PCR based library using a  
 modified protocol from the SMART PCR cDNA Synthesis Kit from  
 Clontech. Directionally cloned into the UDG sites of Pamp1.  
 Dissected nematode tissues were provided by Dr. Alan Scott  
 (ascott@jhsp.h.edu) of the School of Public Hygiene and Public Health  
 at Johns Hopkins University in Baltimore, MD.  
 Seq primer: -40RE from Gibco  
 High quality sequence stop: 58.

FEATURES source

The library was constructed by Brandi Chiapelli and Dr. James  
 McCarter at Washington University, St. Louis. The cDNA was made by  
 using Dynabead Oligo-dT priming (Dynal). PCR based library using a  
 modified protocol from the SMART PCR cDNA Synthesis Kit from  
 Clontech. Directionally cloned into the UDG sites of Pamp1.  
 Dissected nematode tissues were provided by Dr. Alan Scott  
 (ascott@jhsp.h.edu) of the School of Public Hygiene and Public Health  
 at Johns Hopkins University in Baltimore, MD.

Location/Qualifiers

1. .72 /organism="Ascaris suum"  
 /db\_xref="taxon:6553"  
 /clone\_id="Ascaris suum male head pamp1 v2 Chiapelli  
 McCarter"  
 /sex="Male"  
 /tissue\_type="Head"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"  
 /note="Vector: pAMP1 (Gibco); Site\_1: NotI; Site\_2: SalI;  
 The library was constructed by Brandi Chiapelli and Dr. James  
 McCarter at Washington University, St. Louis. The  
 cDNA was made by using Dynabead Oligo-dT priming (Dynal).  
 PCR based library using a modified protocol from the SMART  
 PCR cDNA Synthesis Kit from Clontech. Directionally cloned  
 into the UDG sites of pAMP1. Dissected nematode tissues  
 were provided by Dr. Alan Scott (ascott@jhsp.h.edu) of the  
 School of Public Hygiene and Public Health at Johns Hopkins  
 University in Baltimore, MD.";

BASE COUNT 10 a 22 c 15 g 25 t.

ORIGIN

DEFINITION kh35e05.y1 Ascaris suum male head pamp1 v2 Chiapelli McCarter  
 ACCESSION AZ781553  
 VERSION Az781553.1 GI:12914361  
 VERSION GSS  
 KEYWORD house mouse.  
 SOURCE Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 72)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedernauern,A.,  
 and Wright,D., Weiss,R.  
 TITLE mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah, 125 S. 1500 E., Salt Lake City, UT 84112, USA  
 Tel: 801 585 5605  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0021 row: I column: 03  
 Seq primer: CGTTCTAAACGAGCGCCAGT  
 Class: Plasmid ends  
 High quality sequence stop: 72.  
 FEATURES source

Location/Qualifiers

1. .72 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:0090"  
 /clone\_id="NUGC2Am02103"  
 /clone\_id="Mouse 10kb Plasmid UGGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain X110-Gold, T1-resistant, F-"  
 /note="Vector: pWd42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnare/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWd42 (91147321141gbAF29072.1), a copy-number  
 inducible derivative of plasmid RL. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically competent E. coli X110-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 5 a 26 c 3 g 38 t.

ORIGIN

DEFINITION HS1038-Al-E11-MF.ab1 CIR Human Genomic Sperm Library C Homo  
 sapiens genomic clone Plate=Ctr 820 Col=21 Row=1, DNA sequence.

RESULT 8

B36161/C LOCUS B36161  
 DEFINITION HS1038-Al-E11-MF.ab1 CIR Human Genomic Sperm Library C Homo  
 sapiens genomic clone Plate=Ctr 820 Col=21 Row=1, DNA sequence.

BASE COUNT 100 0% Score 10; DB 13; Length 72;  
 Best Local Similarity 100 0%; Pred. No. 9.5e+04;  
 Matches 10; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

QY 1 CTTCACCT 10  
 Db 26 CTTCACCT 35

BASE COUNT 100 0% Score 10; DB 17; Length 72;  
 Best Local Similarity 100 0%; Pred. No. 9.5e+04;  
 Matches 10; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

QY 1 CTTCACCT 10  
 Db 34 CTTCACCT 43

BASE COUNT 5 a 26 c 3 g 38 t.

ORIGIN

DEFINITION HS1038-Al-E11-MF.ab1 CIR Human Genomic Sperm Library C Homo  
 sapiens genomic clone Plate=Ctr 820 Col=21 Row=1, DNA sequence.

RESULT 9

B36161/C LOCUS B36161  
 DEFINITION HS1038-Al-E11-MF.ab1 CIR Human Genomic Sperm Library C Homo  
 sapiens genomic clone Plate=Ctr 820 Col=21 Row=1, DNA sequence.

ACCESSION B36161  
VERSION B36161.1  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 73)  
AUTHORS Mahairas,G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traioff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.  
TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors  
COMMENT Unpublished (1997)  
Contact: Mahairas GG, Zackrone KD, Hood L  
Seattle, WA 98195, USA  
Tel: (206) 616-8744  
Fax: (206) 685-7301  
Email: kzackr@u.washington.edu  
Sequence Tagged Connector  
Plate: CT 820 row: I column: 21  
Class: BAC ends  
High quality sequence stop: 73.  
FEATURES source  
1 organism="Homo sapiens"  
'/db\_xref="taxon:9606"  
'/clone="Plate:CT 820 col=21 Row=I"  
'/clone\_lib="CIT Human Genomic Sperm Library C"  
'/sex="M"  
'/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"  
BASE COUNT 21 a 14 c  
ORIGIN 21 a 21 g 16 t 1 others  
QY 1 CTTTCACCT 10  
Db 28 CTTTCACCT 19  
  
RESULT 9  
FR0032825  
LOCUS FR0032825  
DEFINITION Fugu rubripes GSS sequence, clone 152F05aG3, genomic survey  
ACCESSION AL029193  
VERSION AL029193.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Takifugu rubripes.  
ORGANISM Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.  
TITLE Direct Submission  
JOURNAL Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biohelp@hgmpr.mrc.ac.uk  
COMMENT Vector: phBlueScript II KS  
V\_type: phagemid  
PRIMER: KS  
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence. Location/Qualifiers  
FEATURES source  
1 organism="Takifugu rubripes"  
'/db\_xref="taxon:31033"  
'/clone="152F05aG3"  
'/clone\_lib="cosmid 152F05"  
BASE COUNT 7 a 22 c  
ORIGIN 7 a 22 c 13 g 35 t 3 others  
QY 1 CTTTCACCT 10  
Db 39 CTTTCACCT 48  
  
RESULT 10  
B1550671  
LOCUS B1550671  
DEFINITION Best Local Similarity 100.0%; Score 10; DB 17; Length 80;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
ACCESSION B1550671  
VERSION B1550671.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 84)  
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausnberg, Ph.D.  
Email: cgabs+@email.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Caninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov/PLAM1695 row: i column: 12  
High quality sequence stop: 84.  
FEATURES source  
1 organism="Homo sapiens"  
'/db\_xref="taxon:9606"  
'/clone="IMAGE:5275475"  
'/clone\_lib="NIH\_MGC\_95"  
'/tissue\_type="hippocampus"  
'/lab\_host="DH10B"  
'/note="Organ: brain; Vector: pBluescript R (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XbaI (gtccat); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTT-3'; size selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carroll, In preparation). Library constructed by M. Brownstein (NHGRI, National Institutes of Health). Note: this is a NIH\_MGC library."  
BASE COUNT 19 a 19 c 30 g 16 t  
ORIGIN 19 a 19 c 30 g 16 t  
QY 1 CTTTCACCT 10  
Db 21 CTTTCACCT 30

RESULT 11		REFERENCE 1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BH405910	BH405910	LOCUS BH405910	88 bp DNA linear GSS 19-APR-2002
DEFINITION RPCI-23-105F8 SP6E RPCI-23 Mus musculus genomic clone RPCI-23-105F8	,	DNA sequence.	
ACCESSION ,			
VERSION BH405910	BH405910.1	GI:17460796	
KEYWORDS GSS			
SOURCE house mouse.			
ORGANISM Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
1 (bases 1 to 88)			
AUTHORS Young, J.M., Friedman, C., Williams, E.M., Ross, J.A., Tonnes-Priddy, L.			
TITLE and Trask, B.J.			
JOURNAL Different evolutionary processes shaped the mouse and human			
MEDLINE Hum. Mol. Genet. 11 (5), 535-546 (2002)			
COMMENT Contact: Young JM			
Barbara Trask, Division of Human Biology			
Fred Hutchinson Cancer Research Center			
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA			
98109-1034, USA.			
Tel: 206 667 1471			
Fax: 206 667 6524			
Email: jayoung@hcrc.org			
Young, J.M., Swartzell, S., Friedman, C., Tonnes-Priddy, L., Lane, R.P.,			
Wallace, J.C., Mahairas, G.G., Hood, L., and Trask, B.J. End sequences			
of mouse BACs containing olfactory receptor genes. Unpublished			
Plate: 105 row: F column: 8			
Seq primer: SP6E			
Class: BAC ends.			
FEATURES source			
1. .88			
/organism="Mus musculus"			
/strain="C57BL/6J"			
/db_xref="taxon:10990"			
/clone="RPCI-23-105F8"			
/clone_id="RPCI-23"			
/sex="Female"			
/lab_host="DH10B"			
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:			
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or			
brain genomic DNA was isolated and partially digested			
with a combination of EcoRI and EcoRI Methylase. Size			
selected DNA was cloned into the pBACE3.6 vector at the			
EcoRI sites. The ligation products were transformed into			
DH10B electrocompetent cells (BRL Life Technologies).			
BASE COUNT 19 a 34 c 11 g 24 t			
ORIGIN			
Query Match 100.0%; Score 10; DB 17; Length 88;			
Best Local Similarity 100.0%; Pred. No. 9.9e+04;			
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 CTTTCACCT 10			
Db 77 CTTCACCT 86			
RESULT 12		RESULT 13	
AZ659166	AZ659166	LOCUS AZ659166	93 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0537H21F Mouse 10kb Plasmid UGC1M library Mus musculus genomic	clone	1M0537H21F, DNA sequence.	
ACCESSION AZ659166	AZ659166.1	VERSION GI:1796912	
VERSION GSS.			
KEYWORDS house mouse.			
SOURCE Mus musculus			
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;			
RESULT 13		REFERENCE 1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AG101870	AG101870	LOCUS AG101870	93 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-105A03.R, genomic survey sequence.			
ACCESSION AG101870	AG101870.1	VERSION GI:16722387	
KEYWORDS GSS.			
SOURCE Pan troglodytes male lymphoblast DNA, clone_id:PTB Chimpanzee Male			
ORGANISM BAC Library clone:PTB-105A03.R.			

		source
REFERENCE		1. .97
AUTHORS		/organism="Homo sapiens"
TITLE		/db_xref="taxon:9606"
JOURNAL		/clone="IMAGE:186192"
REFERENCE		/clone_lib="NCI_CGAP_OV26"
AUTHORS		/sex="female,"
TITLE		/tissue_type="papillary serous carcinoma"
JOURNAL		/dev_stage="adult"
COMMENT		/lab_host="DH10B"
		/note="Organ: ovary; Vector: pAMP1; mRNA made from papillary serous ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."
PRIMERS		
SEQUENCING	M13Rev	
LIBRARY		
VECTOR	: pKS145	
R_SITE_1	: SacI	
R_SITE_2	: SacI.	
FEATURES	source	
BASE COUNT	11 a 34 c 8 g 34 t	1. .93
ORIGIN		/organism="Pan troglodytes"
		/db_xref="taxon:598"
		/clone="PTB-105A3.R"
		/sex="male,"
		/cell_type="lymphoblast"
		/clone_lib="PTB Chimpanzee Male BAC Library"
RESULT	14 a 25 c 11 g 47 t	
BASE COUNT	14 a 25 c 11 g 47 t	
Query Match	100.0%; Score 10; DB 9; Length 97;	
Best Local Similarity	100.0%; Pred. No. 1e-05; Matches 10; Mismatches 0; Indels 0; Gaps 0;	
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 CTTTCACCT 10	
Db	45 CTTTCACCT 54	
RESULT	14	
LOCUS	A1053521	RESULT 15
DEFINITION	q172a0.x1 NCI_CGAP_OV26 Homo sapiens cDNA clone IMAGE:1862006 3', mRNA sequence.	A1053527
ACCESSION	q172a0.x1	DEFINITION
VERSION	A1053527	q172a0.x1 NCI_CGAP_OV26 Homo sapiens cDNA clone IMAGE:1862006 3', mRNA sequence.
KEYWORDS		EST.
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE		Bukarvota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1 (bases 1 to 97)
TITLE		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT		Unpublished (1997)
CONTACT		Contact: Robert Strausberg, Ph.D.
EMAIL		Email: cgs@psr@mail.nih.gov
TISSUE		Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
PROCUREMENT		CNA Library Preparation: David B. Krizman, Ph.D.
VERSION		CNA Library Arrayed by: Greg Lennon, Ph.D.
KEYWORDS		DNA Sequencing by: Washington University Genome Sequencing Center
EST.		Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LNCL at: www.bio.llnl.gov/bgrp/image/Image.html
SOURCE		Seq primer: 40ml3 fwd. ET from Amersham.
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	Homo sapiens	
COMMENT		
REFERENCE	1 (bases 1 to 97)	
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
EMAIL		
TISSUE		
PROCUREMENT		
VERSION		
KEYWORDS		
EST.		
SOURCE		
ORGANISM	H	

Best Local Similarity 100.0%; Pred. No. 1e+05; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCACCT 10  
|||||||  
Db 31 CTTTCACCT 40

Search completed: March 19, 2003, 01:24:57  
Job time : 1328.5 secs